STUDIES ON GENETIC DIVERGENCE, ASSOCIATIONS AND PHENOTYPIC STABILITY OF FODDER YIELD AND ITS COMPONENT CHARACTERS IN OAT (*Avena sativa* L.)

Thesis Submitted to the Bundelkhand University, Jhansi in fulfillment of the requirements for the Degree of

DOCTOR OF PHILOSOPHY IN GENETICS AND PLANT BREEDING

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Dedicated to

My

Beloved Parents

Whose blessing brought
me here upto

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CERTIFICATE

This is to certify that this dissertation entitled, "**Studies on genetic divergence, associations and phenotypic stability of fodder yield and its component characters in oat (*Avena sativa* L.)**" submitted for the degree of **Doctor of Philosophy** in the subject of **Genetics and Plant Breeding** to the **Bundelkhand University, Jhansi,** is a bonafide research work carried out by **Mr. Raj Bahadur** under my supervision and that no part of this dissertation has been submitted for any other degree. The assistance and help received during the course of investigation have been fully acknowledged.

I, further certify that:

- It embodies the original work of candidate himself.
- It is up to the required standard both in respect of its contents and literary presentation for being referred to the examiners.
- The candidate has worked under me and has put in required attendance in Crop Improvement Division, IGFRI, Jhansi, during the course of investigation.

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DECLARATION

I, hereby declare that the dissertation entitled "**Studies on genetic divergence, associations and phenotypic stability of fodder yield and its component characters in oat (*Avena sativa* L.)**" being submitted for the degree of Doctor of Philosophy in Genetics and Plant Breeding to Bundelkhand University, Jhansi, is an original piece of research work done by me under the supervision of Dr.R.N.Choubey, Principal Scientist (Plant Breeding) and Head, Division of Crop Improvement, IGFRI, Jhansi, and to the best of my knowledge, any part or whole of this thesis has not been submitted for a degree or any other qualification of any university or examining body in India/elsewhere.

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CHAPTER-I

INTRODUCTION

INTRODUCTION

Oat (*Avena sativa* L.), one of the important cereals, is a dual-purpose crop of temperate and sub-tropical areas. Being a highly nutritious cereal, it is used for human consumption as well as feed and fodder for dairy and other animals. In India, oat is exclusively grown for fodder in western Uttar Pradesh, Haryana and Punjab. It is also grown on limited scale in some parts of Maharashtra, Madhya Pradesh, Gujarat, Orissa, Bihar and West Bengal. Among winter forages, it contains relatively higher dry matter content with 7-10 per cent protein and resistance to diseases and is most suited for silage. With minimum irrigation it gives high fodder yield per unit area per unit time due to its multicut nature which ensures regular supply of fodder over a long period of time (Solanki, 1977). With these merits and development of an intensive livestock industry in the country in recent years, it has now gained much importance as a forage crop. Performance of our livestock for milk, meat and wool is the lowest in the world inspite of 480 million of its population. The main reasons for the lowest performance of livestock in our country are due to poor genetic potential and under nutrition. However, the genetic potential of livestock has been improved to a larger extent but their under nutrition still persists.

The country accounts for 15 per cent of the world's livestock population with only 2 per cent of the total world's geographical area due to which the deficiency in the total forage availability is about 53 per cent for dry and about 68 per cent for green fodder (Paroda, 1992). This deficit is likely to increase further, because of the burgeoning livestock population and depleting land availability for forage crops. This has created a situation where animals are unable to get even one-third of what they need for maintenance ration of 6.0 kg

of roughage and 3.6 kg of green fodder per day for a body weight of 300 kg. Therefore, looking at the vast gap between the demand and supply position, development of superior varieties/hybrids offers solution to the problem of sustained and increased fodder supply per unit area and time particularly where economy of the farmer is based on mixed farming system.

There are high yielding fodder crops and grasses during kharif season to meet the requirement of fodder but during winter season, the scope is limited to berseem in irrigated areas and oats in areas where the irrigation facilities are limited. Oat like other forage crops is generally grown in varied agroclimatic and fertility conditions. The biomass productivity of forages including oat by and large, fluctuates with the change of environment. In order to have consistency in forage yield performance of a variety over environments, development of stable genotypes associated with high production potential appears to be obligatory. Perkins and Jinks (1968a) proposed joint regression analysis which has been a widely acceptable approach for finding out the stability of genotypes.

To boost up further productivity of forage oats, it has been envisaged that hybridization and exploitation of heterosis may play significant role in coming years. For developing better genotypes through hybridization, the choice of suitable parents is a matter of great concern to the plant breeders. For this purpose, it is essential to quantify the genetic diversity among the parents. The more diverse the parents, the greater are the chances of achieving heterotic F_1's and wide spectrum of transgressive segregants in segregating generations. There are various reports indicating that the genetic diversity may not be associated with geographical diversity. Mahalanobis D^2 statistics is adopted to identify the diverse groups of genotypes for hybridization purposes.

To initiate effective selection programme at early stages for further advancement in fodder yield of oat, it is necessary to know about interrelationship among fodder yield components and quality traits in order to discard the undesirable types based on these traits and to include those traits as a selection criteria in forage oat improvement programme. The detailed information on genetic divergence, association and phenotypic stability in forage oats is hardly available. In view of this, the present investigation was conducted in forage oats with the following objectives:

1. To study the variability and genetic divergence amongst various strains of different geographical origin using D^2 statistics.
2. To investigate the associations of different characters among themselves and their direct and indirect effects on fodder yield.
3. To identify the differential response of various genotypes over different environments and to find out stable genotypes.

CHAPTER-II

REVIEW OF LITERATURE

REVIEW OF LITERATURE

Oats, being highly nutritive and palatable crop is becoming popular among the farmers for both fodder and grain in India. Most of the work has been done to develop high yielding single and multicut varieties. However, the limited work on genetic divergence, association and stability aspects vis-à-vis genotype x environment effect has been done particularly on fodder quality parameters. Therefore, the information available on these aspects on oat is reviewed under the following sections:

2.1 Genetic variability

2.2 Genetic divergence

2.3 Association and path-coefficient analysis

2.4 Phenotypic stability

2.1 GENETIC VARIABILITY

Availability of genetic variability for the component characters is a major asset for initiating a fruitful crop improvement programme. Infact, plant breeding has amply been defined as a purposeful management of variability. Since whole breeding pursuit relates to the creation and management of genetic variability, the proper information on this aspect in the material is a pre-requisite before embarking on any breeding method. Finlay (1971) has stressed the importance of continuous infusion of new genetic variability in active plant breeding programmes. There is constant search for new, diverse and useful genetic stocks for improving and stabilizing quantity and quality of produce. Continuing the efforts in this direction numerous investigators have reported adequate variability in forage oats for following different characters.

Characters	References
Days to 50% flowering	Singh and Katoch (1975), Nehvi Shafiq *et al.* (2000).
Plant height	Bhagmal *et al.* (1975), Singh and Katoch (1975), Nair and Gupta (1977), Choubey and Gupta (1986), Rahaman and Roquib (1987), Bahl *et al.* (1989), Kumar *et al.* (1995), Singh (1999), Nehvi Shafiq *et al.* (2000).
No. of tillers/ plant	Nair and Gupta (1977), Rahaman and Roquib (1987), Kumar *et al.* (1995), Singh (1999).
Stem diameter	Bhagmal *et al.* (1975), Rahaman and Roquib (1987), Kumar *et al.* (1995).
No. of leaves/ plant	Singh and Katoch (1975), Nair and Gupta (1977), Kumar *et al.* (1995), Singh (1999), Nehvi Shafiq *et al.* (2000).
Leaf length	Bhagmal *et al.* (1975), Nair and Gupta (1977), Rahaman and Roquib (1987), Kumar *et al.* (1995).
Leaf breadth	Bhagmal *et al.* (1975), Nair and Gupta (1977), Rahaman and Roquib (1987), Kumar *et al.* (1995).
Leaf: stem ratio	Kumar *et al.* (1995), Singh (1999).
Green fodder yield/plant	Bhagmal *et al.* (1975), Choubey and Gupta (1986), Rahaman and Roquib (1987), Singh (1999), Nehvi Shafiq *et al.* (2000).
Dry fodder yield/plant	Singh and Katoch (1975), Nair and Gupta (1977), Rahaman and Roquib (1987), Bahl *et al.* (1989), Kumar *et al.* (1995), Singh (1999).
Protein content	Hosoya *et al.* (1998).
IVDMD	Hosoya *et al.* (1998).

2.1.1 Heritability and genetic advance:

Several workers worked out heritability and genetic advance in oats and the trend of their findings is given as under:

Characters	Heritability	Genetic advance	References
Days to 50% flowering	High	High	Srivastava *et al.* (1995).
	High	Low	Nehvi Shafiq *et al.* (2000).
Plant height	High	High	Bhagmal *et al.* (1975), Nair and Gupta (1977), Choubey and Gupta (1986), Bahl *et al.* (1989), Srivastava *et al.* (1995), Singh (1999), Nehvi Shafiq *et al.* (2000).
	Moderate	-	Rahaman and Roquib (1987).
No. of tillers/ plant	High	High	Nair and Gupta (1977), Singh (1999).
	Low	-	Rahaman and Roquib (1987).
Stem diameter	Moderate	-	Rahaman and Roquib (1987).
No.of leaves/ plant	High	High	Nair and Gupta (1977), Singh (1999), Nehvi Shafiq *et al.* (2000).
	Moderate	-	Rahaman and Roquib (1987).
Leaf length	High	High	Nair and Gupta (1977).
	Moderate	-	Rahaman and Roquib (1987).
Leaf breadth	High	High	Nair and Gupta (1977).
	Low	-	Rahaman and Roquib (1987).

Leaf: stem ratio	High	High	Srivastava *et al.* (1995), Singh (1999).
Green fodder yield/plant	High	High	Bhagmal *et al.* (1975), Choubey and Gupta (1986), Srivastava *et al.* (1995), Singh (1999), Nehvi Shafiq *et al.* (2000).
	Moderate	Low	Singh and Katoch (1975).
	Low	-	Rahaman and Roquib (1987).
Dry fodder yield/plant	High	High	Nair and Gupta (1977), Bahl *et al.* (1989), Srivastava *et al.* (1995), Singh (1999).
	Low	-	Rahaman and Roquib (1987).
Protein content	High	-	Manga and Sidhu (1980).
	Moderate	-	Stuthman and Marten (1972).
IVDMD	Moderate	-	Stuthman and Marten (1972).

2.2. GENETIC DIVERGENCE

The importance of genetic divergence for improving yield potential, *per se* through hybridization has been emphasized by several authors and reviewed by Frey (1971). Although, it has long been appreciated by breeders, the basic difficulty has always been one of recognizing and reliable estimation of such diversity without making actual crosses (Bhatt, 1970). Since most of the quantitative characters are highly influenced by environments, it becomes difficult to separate non-heritable components from heritable components of variability based on phenotype.

In the past, geographical distance of species and varieties has often been considered as a criterion for the measures of genetic diversity (Dhawan and Singh, 1961; Moll *et al.*, 1962; Singh and

Joshi, 1966) but it was over ruled by Somayajulu *et al.* (1970), Jayaprakash *et al.* (1974) and Chandra (1977). Therefore, a technique which can provide direct and reliable estimates of diversity at genetic level will obviously be more useful. Hutchinson's polygraph (Hutchinson, 1936) and metroglyph and index score analysis (Anderson, 1957) broadly classified the germplasm but they did not provide numerical estimates for precise comparison. Discriminant function originally suggested by Fisher (1936), is a useful criterion to select the best individuals from populations based on single parameter. However, the situation becomes difficult when the number of variables to be considered is increased. Pearson (1926) suggested the coefficient of racial likeness (CRL) as a single numerical measure, which would express the degree of resemblance or divergence of two races when several characters were measured on relatively few individuals from either or both the races. Rao (1948) pointed out that CRL was an imperfect tool because it neglects correlations between characters under study.

Mahalanobis (1925) gave the concept of generalized distance based on second degree statistics and it is self weighing on the basis of genetic variability. Mahalanobis (1928) commented that CRL was a 'test' of divergence between two samples rather than an actual measure of magnitude of genetic divergence and it would be logical to use measure and not the test of divergence for quantitative comparisons between the populations. Mahalanobis (1930) for the first time applied his D^2 statistics on the extensive measurement of Swedish population. In anthropological survey of united province this technique was further applied (Mahalanobis, 1949).

Mahalanobis's D^2 statistics can be successfully used for genetic divergence studies due to the following reasons:

i. D^2 statistics provides a numerical estimate and permits precise comparisons among all possible pairs of populations.

ii. Effects of correlation among various characters of the population are removed during computation of this estimate.

iii. D^2 technique is based on second-degree statistics with automatic weightage of each character.

iv. It helps in grouping of strains on the basis of magnitude of diversity among them.

v. Relative contribution of each character towards total genetic diversity can also be measured.

vi. This technique helps to select the diverse parents for hybridization programme.

Rao (1952) described D^2 statistics as a measure of actual divergence between any pair of populations which amounts to a measure of genetic divergence and in 1960 he suggested the use of D^2 statistics in genetic problems. Murty and Pavate (1962) were the first to use this approach for the study of genetic divergence. Murty and Arunachalam (1966) hypothesized that Mahalanobis D^2 statistic could be useful multivariate tool for effective discrimination among parents on the basis of genetic diversity. The potential of using Mahalanobis D^2 distance for parental selection has amply been assessed by Bhatt (1970). From these studies, it may be concluded that:

1. Geographical diversity may not necessarily be related with genetic diversity.
2. The potent factors responsible for diversity are fitness characters as the artificial selection during the course of evolution of varieties has been practised for such characters.
3. Parentage has some effect on the spatial position of clusters.
4. Composition of clusters differed from environment to environment.

After that, using D^2 statistics, several workers have successfully grouped the populations into the different clusters in various crops. In forage oat, only sporadic reports are available on this aspect.

Nair and Gupta (1977) classified 32 varieties of oat into 14 groups on the basis of plant height, tiller number, leaf area and leaf number with the aid of the Mahalanobis's D^2 statistics. Groups IV, VI, VII, IX and XII, each containing one variety except group VI which contained four varieties, were more divergent than the others with respect to tiller number and leaf area and leaf number, and hence, these would be of value in breeding for increased fodder yield.

Sidhu and Mehndiratta (1981) by multivariate analysis in 30 indigenous and exotic varieties of oats found 11 clusters which indicated existence of wide genetic divergence in the material. The number of tillers contributed most to the genetic divergence, followed by plant height and leaf width. Genetic diversity did not reflect geographical diversity. The varieties adapted to the particular climatic condition result in almost same magnitude of genetic divergence regardless of their geographical distribution.

Pukhal' Skii *et al.* (1990) estimated genetic divergence for 8 yield related traits in 8 Soviet and foreign varieties of oat using the D^2 statistics. Significant differences between varieties were found for the traits. All the genotypes were grouped in 3 clusters. No clear association was detected between the genetic divergence of varieties and their geographical origin. They suggested that for breeding purposes, the varieties should be selected from each cluster with values exceeding the mean of the cluster for the greater number of traits.

Bedis and Patil (1993) found considerable genetic diversity for green forage yield per plant and 10 related characters among 54 strains of forage oat using Mahalanobis's D^2 statistic. The strains were grouped into 18 clusters and the clustering pattern revealed that

genetic divergence was not necessarily associated with geographical diversity. The hybridization programme, on the basis of inter-cluster divergence, cluster means and *per se* performance for the characters studied has been suggested.

Kishor *et al.* (1996) studied genetic divergence for fodder yield and its related traits in 44 diverse strains of oats under normal and late sown conditions using D^2 techniques. The genotypes were grouped in 12 clusters in E_1 and in 9 clusters in E_2 . There was no association between clustering pattern and ecogeographical distribution of the genotypes.

Babbar *et al.* (1997) studied relationship of parental diversity and heterosis for yield in 8 oat lines crossed with 4 testers in 32 hybrid combinations using Mahalanobis D^2 analysis. Parental diversity had no relationship with heterobeltiosis for these traits, indicating that selection of parents based on genetic diversity will not be effective. Utility of genetically diverse parents in hybridization programme has been emphasized by them in the genetic improvement of oats.

Dubey *et al.* (2000) made 9 clusters out of 90 genotypes of oat for 11 developmental characters using D^2 statistic. Distribution of different genotypes in different clusters possessed considerable diversity within and between groups, which could be exploited in breeding programme.

Choubey *et al.* (2001) grouped 300 germplasm lines of oat into 14 clusters using D^2 statistic and reported that the diversity among the genotypes measured by inter-cluster distance was adequate for improvement of forage oat by hybridization and selection.

2.3 ASSOCIATION AND PATH-COEFFICIENT ANALYSIS

Yield is a complex character and improvement in it largely depends upon the improvement of its component characters. It, therefore, becomes essential to know the associations of the various

quantitative characters with yield in order to develop the guidelines for improvement in yield of a crop. However, correlation coefficients, do not give a complete picture of a rather complex situation as these measure the association between two characters only. But path-coefficients suggested by Wright (1921) furnishes a means of untangling direct and indirect contribution of various factors involved in building up a complex correlation. The utility of path-coefficient analysis in plant selection was demonstrated by Dewey and Lu (1959) in 81 crested-wheat grass progenies.

Stuthman and Marten (1972) observed that forage yield and quality were negatively correlated with digestibility and heading in oat.

Singh and Katoch (1975) found that dry matter yield was highly and positively correlated with number of days to 50% flowering, plant height and leaf number, whereas, negatively correlated with leaf: stem ratio. Significant positive genotypic and phenotypic correlations occurred between green fodder yield and plant height, stem girth, leaf length and leaf width, but significant negative genotypic and phenotypic correlations occurred between green fodder yield and days to bloom and leaf number (Bhagmal *et al.*, 1975).

Dhumale and Mishra (1979) found that green forage yield was positively correlated with plant height, flag leaf width and number of tillers per plant. Number of tillers per plant was negatively correlated with plant height and days to 50 per cent heading. Path-coefficient analysis indicated that plant height had a considerable direct effect on green forage yield.

Choubey and Gupta (1986) showed that green forage yield was highly and positively correlated with plant height, leaf length, leaf breadth and stem diameter. Plant height and leaf breadth had large and positive direct effects on green forage yield.

Bahl *et al.* (1988) reported positive associations among dry matter yield per plant, green fodder yield per plant, dry matter yield per day and green fodder yield per day. Green fodder yield per plant was positively associated with stem thickness and leaves per plant. Path coefficient analysis revealed that magnitude and sign of direct and indirect effects of fodder yield contributing characters varied considerably over different environments.

Dubey *et al.* (1995) found that plant height, number of leaves per plant, leaf area per plant, tillers per plant and stem thickness had a positive relationship with fodder yield.

Srivastava *et al.* (1995) observed that green and dry fodder yield were highly associated with days to 50 per cent flowering, plant height, stem girth, number of tillers, number of leaves, leaf length, leaf breadth and leaf: stem ratio both in parental and F_2 populations at both phenotypic and genotypic level. Path-coefficient analysis revealed that plant height, number of leaves, leaf size and leaf: stem ratio had high direct positive effects on fodder yield in both parental and F_2 populations.

Singh and Nanda (1998) reported that green forage yield was positively correlated with plant height, number of tillers and leaf: stem ratio, whereas crude protein was negatively correlated. Green fodder yield exhibited a significant positive correlation with plant height, number of leaves per plant, green leaf and stem weight per plant. Path-coefficient analysis indicated that green leaf weight and green stem weight were the major determinants of fodder yield (Nehvi Shafiq *et al.*, 2000).

Choubey *et al.* (2001) reported that tiller number, number of leaves and flag leaf length were main traits for selection of high yielding types in forage oat.

2.4 PHENOTYPIC STABILITY

2.4.1 Role of G x E interaction in plant breeding:

A specific genotype does not exhibit the same phenotypic expression under all environments. Different genotypes respond differently to a specific environment. This variation arising from the lack of correspondence between the genetic and non-genetic causes, is known as genotype x environment (G x E) interaction. Therefore, a phenotype is the result of an interplay of a genotype and its environment. The interactions are widely present and contribute substantially to the non-realization of expected gains from selection (Comstock and Moll, 1963) and thus obstruct the progress of breeding programmes.

Johannsen (1909) was one of the earlier workers to recognize the importance of environment in the developmental process. His work paved the way to a greater understanding of those processes by which genotype and the environment jointly regulate the development of a particular individual. Frankel (1958) suggested two steps to minimize G x E interactions: (i) stratification of environments, and (ii) breeding of stable varieties. However, further studies have exhibited that even stratification of environment does not aid in reducing G x E interaction. Therefore, evolving of stable varieties received considerable significance in plant breeding programmes.

Finlay and Wilkinson (1963) reported that the plant breeders although were aware of the importance of genotypic differences in adaptability, they were not able to exploit them fully in breeding and measuring either adaptability itself or the complexities of natural environment. They defined that an ideal variety is one that combines the maximum potential in the best environment with maximum stability and the least/low genotype x environmental interactions.

Allard and Bradshaw (1964) have found that environmental variation could be of two types: predictable and unpredictable fluctuations in the environment. Therefore, the G x E interaction plays an important role in the management of genetic variability.

In the past, several studies have been conducted on genotype x environment interactions and the most significant advances in biometrical genetics during the last three decades have been made in the field of genotype x environment interactions. These interactions were termed as instabilities and the main efforts were in the direction of reducing them or in trying to extract them. Further, as the number of genes involved in the inheritance of an attribute becomes larger, the opportunity for influence by environment also increases (Gamble 1962; Shebeski and Evans, 1973) thus, complicating the process of evaluation.

2.4.2 Estimation of phenotypic stability and adaptability:

An early attempt was made by Yates and Cochran (1938) to obtain the measurement of stability of individual genotype on the basis of regression technique. Plaisted and Peterson (1959) suggested method to characterize the stability of yield performance when several varieties were tested at a number of locations within a year. This method, however, proved to be of limited utility in plant breeding programme as a large number of analysis are required, i.e., n(n-1)/2 for n varieties.

Finlay and Wilkinson (1963) reported relatively simple and dynamic approach to describe the environments and to measure the adaptability of varieties. They used the average yield performance of all the varieties for quantification of the environment. Mean and regression coefficient value were used to determine the adaptability of varieties. In this technique, the linear regression of yield of each variety on the mean yield of all the varieties in each environment

provides the measure of phenotypic stability. An ideal variety was defined as one with high mean and unit regression coefficient.

Eberhart and Russell (1966) modified the above technique by adding another stability parameter namely, the deviation from regression ($S^{-2}d_i$). They considered that the most desirable variety is one which has high mean yield ($\bar{X}$), unit regression coefficient (b=1.0) and least deviation from the regression ($S^{-2}d_i = 0.0$). These two approaches by these workers were purely statistical. The other approach, which is genetical, was given by number of workers (Mather and Jones, 1958; Jinks and Stevens, 1959; Bucio-Alanis, 1966; Bucio-Alanis and Hill, 1966).

Perkins and Jinks (1968a) tried to reduce the gap between statistical and genetical approaches by expressing the expectations of statistical analysis in terms of standard model of genotype environment interaction and have extended the Bucio-Alanis analysis to cover many inbred lines and crosses among them. They concluded that while a significant proportion of genotype x environmental interaction component of variation was a linear function of the environmental component but there was still a significant non-linear component.

Perkins and Jinks (1968b) reviewed the non-linear component of the interaction by grouping varieties into homogeneous groups on the basis of deviation from linear regression and reported a significant reduction in the non-linear component of the interaction as a result of grouping of varieties. They found that the various component of phenotype, mean performance, linear and non-linear components of G x E interactions and within environment component are independent and presumably under the control of different genetic systems.

Breese (1969) and Samuel *et al.* (1970) reported that linear regression (bi) should be regarded as a measure of response of a

particular genotype, whereas, deviation from linear regression should be considered as a measure of stability.

The independent assessment of environmental index was proposed by Freeman and Perkins (1971) who reviewed the techniques and advocated that various multivariate techniques may be used to assist in the elucidation of interaction, especially when these are not easy to explain by simpler method of analysis.

Cooper *et al.* (1993) suggested the advanced techniques in the study of G x E interaction and their application to plant breeding and developed a descriptive framework for considering G x E interaction to show how they make impact on response to selection and how an understanding of G x E interaction is to be applied in plant breeding, particularly in designing selection strategies.

2.4.3 Genotype x Environment interactions in oats:

Several workers have worked out stability of genotypes in forage oats and the references pertaining to phenotypic stability are reviewed here:

Paroda *et al.* (1973) reported significant linear and non-linear components of G x E interactions for green fodder yield in 10 genotypes of oats. The magnitude of non-linear component was considerably smaller than that of linear component. Genotypes 37/14, 5/104, "Mulga" and "Fulgham" were found to be most stable and thus their response to change in environments could be predicted.

Pfahler and Linskens (1979) studied the relationship between yield stability and population of oats containing various numbers and combinations of diverse homozygous and homogeneous lines and indicated that multilines gave satisfactory yield and displayed enhanced yield stability.

Kumar *et al.* (1982) observed that both linear and non-linear components of G x E interactions were highly significant for all the characters in oats. However, linear portion was significantly higher

for days to 50 per cent flowering and number of tillers per plant, whereas non-linear portion was more for green fodder yield. Genotype OS-6 showed general adaptability to all the environments for green fodder yield, whereas OS-5, OS-8 and OS-9 were specially suited to favourable environments and OS-54 was specially suited for unfavourable environments. These genotypes were also stable for other characters and therefore, appeared to hold promise.

Singh *et al.* (1984) revealed that both linear and non-linear components contributed equally to total G x E interaction for protein content in oats. The cultivars, Weston-11 and OS-77 were specially suited to poor and better environments, respectively. Adegoke and Frey (1987) observed that high yielding lines were the most responsive to good environments and were the most stable.

Prakash *et al.* (1989) investigated both linear and non-linear components of G x E interactions. Non-linear portion was higher than linear portion. Genotypes OS-152, OS-6, OS-119, OL-77 and OS-154 were high yielders. Out of these, OS-119 was suited to favourable environments, while other genotypes were suited to a wide range of environments. The genotype, HFO-149 was suitable for poor environments.

Prakash and Kishor (1990) reported significant G x E interaction for protein content in oats. Linear portion was non-significant, while non-linear portion of G x E interaction was highly significant. Genotypes OS-154 and HFO-245 had above average response indicating their suitability to better environments. Genotype OS-86 had below average response and could be exploited in poor environments.

Nandanwar *et al.* (1990) studied stability performance of 10 oat varieties for fodder and reported that genotypes OL-9, OL-88 and Kent were stable for green and dry fodder yield. Thaware *et al.* (1992) reported significant G x E interactions for green forage yield in oats.

The stable genotypes OL-125, JHO-817, UPO-206 and OL-6 may be used in breeding programme for increasing forage production.

Singh *et al.* (1992) made a comparative study for identification of promising and stable oats strains for their forage production under different agro-climatic zones. G x E interactions were found highly significant in all the cases. The cultivars OS-121, OL-244, OL-265, UPO-206, OS-96, JHO-817 and Kent for North-West zones; OS-96, OS-6 and JHO-817 for North-East zones; UPO-206, JHO-817, OS-6 and OS-129 for Central zone and JHO-817 for all India level were found stable and high yielding.

Kishor *et al.* (1994) observed significant genotype x environment interactions for few morphological traits in 44 genotypes of oats. The genotypes OS-6, OL-77, OS-152 and OS-119 were found good in their performance and better suited in all types of environments.

Dubey *et al.* (1995) studied stability in 90 diverse genotypes of oats grown under different environments and found that genotypes JHO-330, OL-88, Palampur, JHO-829 and UPO-224 were best suited for poor environments; OL-9, OS-8 and UPO-222 were best suited for normal conditions and OL-89, OL-60 and K-353 were best performers under high input conditions.

Gupta and Singh (1997) observed that magnitude of the linear component was higher than that of the non-linear component and only the linear component was important for green fodder yield. Genotypes OS-137, OS-145, OS-148, PLP-1 and OL-9 were superior and stable for green fodder yield, while OL-9 and OS-145 were best for dry matter yield.

Babbar *et al.* (1998) revealed that the variety Kent showed good stability for majority of fodder characters. OS-7, a high fodder yielding genotype was found suitable for favourable environments,

whereas OL-88, OS-96 and Sierra performed well under a wide range of environments.

Pundir *et al.* (2002) reported significant linear and non-linear components of G x E interaction for green and dry fodder yield in oats. The magnitude of linear component was higher for both the traits. Genotypes OS-6, OS-96, JHO-996, JHO-822 and UPO-238 were found stable and high fodder yielding.

CHAPTER-III

MATERIALS AND METHODS

MATERIALS AND METHODS

3.1 MATERIALS

The experimental material for the present investigation, comprising 50 diverse genotypes and elite breeding lines of forage oats (*Avena sativa* L.), was collected from Division of Crop Improvement, IGFRI, Jhansi and Forage Research Section, Department of Plant Breeding, CCS HAU, Hisar (Table 1).

Table 1: List of 50 genotypes of oats

	Genotypes	Origin/source		Genotypes	Origin/source
1.	Kent	Australia	26.	JHO-99-7	IGFRI, Jhansi
2.	DFO-54	NBPGR, New Delhi	27.	Blacknip	-do-
3.	DFO-57	-do-	28.	S-2688	-do-
4.	JHO-94-1	IGFRI, Jhansi	29.	S-3021	-do-
5.	JHO-94-3	-do-	30.	UPO-212	GBPUAT, Pantnagar
6.	JHO-95-1	-do-	31.	UPO-230	-do-
7.	JHO-95-2	-do-	32.	UPO-248	-do-
8.	JHO-96-4	-do-	33.	UPO-250	-do-
9.	JHO-96-6	-do-	34.	UPO-288	-do-
10.	JHO-97-4	-do-	35.	OL-661	PAU, Ludhiana
11.	JHO-810	-do-	36.	OL-805	-do-
12.	JHO-822	-do-	37.	OL-936	-do-
13.	JHO-829	-do-	38.	OS-6	CCS HAU, Hisar
14.	JHO-851	-do-	39.	OS-7	-do-
15.	JHO-866	-do-	40.	OS-174	-do-
16.	JHO-889	-do-	41.	OS-189	-do-
17.	JHO-897	-do-	42.	OS-237	-do-
18.	JHO-995	-do-	43.	OS-242	-do-
19.	JHO-851Elite	-do-	44.	OS-245	-do-
20.	JHO-99-1	-do-	45.	OS-277	-do-
21.	JHO-99-2	-do-	46.	OS-279	-do-
22.	JHO-99-3	-do-	47.	OS-285	-do-
23.	JHO-99-4	-do-	48.	OS-286	-do-
24.	JHO-99-5	-do-	49.	HJ-8	-do-
25.	JHO-99-6	-do-	50.	HFO-114	-do-

3.2 EXPERIMENTS

The above experimental material was planted at the research area of the Division of Crop Improvement, Indian Grassland and Fodder Research Institute, Jhansi (25°27N′ lat., 78°35′E long., 271 m alt.) and Forage Research Section, Department of Plant Breeding,

CCS Haryana Agricultural University, Hisar (29°10N' lat., 75°46'E long., 215 m alt.) during 1999-2000 under normal and late sown conditions according to the details given in Table 2. Each genotype was grown in a randomized block design with three replications in two rows of 4 m length spaced 30 cm between rows and 10 cm between plants. All the normal cultural practices as recommended for oat cultivation were adopted throughout the crop season.

Table 2: Description of environments

Environments	Location	Date of sowing	Sowing season
E_1	IGFRI, Jhansi	Nov. 26, 1999	Normal sown
E_2	IGFRI, Jhansi	Dec. 26, 1999	Late sown
E_3	CCS HAU, Hisar	Nov. 19, 1999	Normal sown
E_4	CCS HAU, Hisar	Dec.19, 1999	Late sown

3.3 WEATHER DATA

Monthly weather data relating to temperature, relative humidity, sunshine and rainfall during the crop season at both the locations are given in Table 3.

Table 3: Monthly meteorological data during crop season at Jhansi and Hisar

Month	Location	Temperature (°C)		Relative humidity (%)		Sunshine (hrs)	Rainfall (mm)
		Max.	Min.	M	E		
Nov.,1999	Jhansi	30.8	11.7	88.3	31.5	9.0	0.0
	Hisar	30.4	9.0	75.5	21.9	8.1	0.0
Dec.,1999	Jhansi	24.9	6.9	93.4	36.8	7.6	0.0
	Hisar	23.6	3.7	89.9	38.0	6.1	0.0
Jan.,2000	Jhansi	24.3	6.7	92.2	37.0	8.6	0.0
	Hisar	18.8	5.9	91.2	61.4	5.2	1.9
Feb.,2000	Jhansi	25.6	7.2	91.0	36.0	9.2	0.0
	Hisar	20.8	5.9	92.5	59.5	8.8	2.4
Mar.,2000	Jhansi	33.5	12.1	81.6	26.8	10.1	0.0
	Hisar	30.7	10.2	75.6	26.2	9.1	0.0
Apr.,2000	Jhansi	41.1	21.9	57.8	18.8	9.4	0.4
	Hisar	40.6	19.7	48.8	15.5	9.3	0.0

Source: Department of Meteorology, IGFRI, Jhansi and CCS HAU, Hisar.

3.4 OBSERVATIONS RECORDED

Five competitive plants excluding border plants in each genotype were randomly selected from each replication in each environment. Data on individual plants were recorded for the following fodder attributes.

3.4.1 Days to 50% flowering: Number of days was taken from the date of sowing to the date of 50 per cent flowering of each genotype.

3.4.2 Plant height (cm): The height of the main shoot of five plants, on the day of 50 per cent flowering was measured in centimeters as the distance from the base of the main shoot to the base of the lamina of the last leaf and averaged.

3.4.3 Number of tillers/plant: All the tillers, which came out from the base, including main tiller of five plants, were counted and averaged.

3.4.4 Stem diameter (mm): The diameter of the main tillers of five competitive plants was recorded in milimeter at the third internode from the top using electronic caliper and averaged.

3.4.5 Number of leaves/plant: Total number of leaves of all the five plants were counted and averaged.

3.4.6 Leaf length (cm): The leaf length was measured in centimeters along the mid-rib of the third leaf from the top of the main tiller of five plants and averaged.

3.4.7 Leaf breadth (cm): Leaf breadth was measured in centimeters at the point of maximum breadth of the leaves of main tiller of five plants. The same leaves, which were used for leaf length, were used for this observation and averaged.

3.4.8 Leaf: stem ratio: Leaf: stem ratio was worked out by dividing green leaf weight (green portion) of all the leaves with green stem weight (along with leaf sheath) of five plants and averaged.

3.4.9 Green fodder yield/plant (g): The sum of weight of green leaves and stems of five plants was recorded in grams and averaged.

3.4.10 Dry fodder yield/plant (g): The samples of green leaves and green stem were oven dried. Dry leaf weight/plant and dry stem weight/plant of the same plant were added to record dry fodder yield/plant in grams and averaged.

3.4.11 Crude protein content (%): Analytical method proposed by Mc Kenzie and Wallace (1954) was used. The oven dried 100 mg of ground sample was taken in Kjeldahl digestion flask, a pinch of catalyst mixture of $CuSO_4$ and K_2SO_4 in 1:10 ratio was added. To this, 10 ml of conc. H_2SO_4 was added and the sample was digested. After cooling the digested sample, the volume was made up to 100 ml with distilled water. From this, 10 ml aliquot was taken and dropped in micro Kjeldahl distillation apparatus followed by 10 ml of 40 per cent NaOH solution for distillation. Thus, ammonia liberated was absorbed in N/100 H_2SO_4 solution. Then it was titrated against N/100 NaOH using Methyl red as an indicator and the amount of nitrogen was calculated as:

1 ml of N/100 H_2SO_4 = 0.00014 g N

$$\text{Nitrogen (\%)} = \frac{\text{Volume of N/100 } H_2SO_4 \text{ used x } 0.00014}{\text{Aliquot taken x weight of sample}} \text{ x } 100$$

Crude protein (%) = Nitrogen (%) x 6.25

3.4.12 *In vitro* dry matter digestibility (IVDMD) (%): The method of Barnes *et al.* (1971) was used for determining the *in vitro* dry matter digestibility of fodder samples. *In vitro* system consisted of 250 mg samples of substrate in test tube fitted with gas release valve. The buffer-nutrient solution added to each tube was 25 ml of CO_2 saturated phosphate carbonated buffer (pH 7.0) and then followed by 5 ml of strained rumen fluid per tube served as inoculum. Blank tubes

were included to which only buffer nutrient solution and rumen fluid were added. The tubes were immediately stoppered and incubated in an incubator at 37±1°C. Standard samples of known IVDMD were run in triplicate with each set. Tubes were shaken gently thrice daily during incubation period to resuspend the substrate. After 48 hours, 2 ml of 6 N HCl and 0.1 to 0.2 g of Pepsin powder were added to each tube and mixed thoroughly. The tubes were incubated for an additional 48 hours and filtered through weighted Whatman No.54 filter paper. The tubes were rinsed and washed with boiling distilled water. The residue on the filter paper was dried overnight at 90°C and weighed for determining the digestibility. IVDMD percentage was calculated as follows:

$$\text{IVDMD (\%)} = \frac{250 \text{ mg} - \left[\text{Dry matter of residue (mg)}\right] - \left[\text{Dry matter of blank (mg)}\right]}{250 \text{ mg}} \times 100$$

3.5 STATISTICAL ANALYSES

Mean values of the five selected plants from each replication were utilized for all the characters. After testing the homogeneity of error variances using Bartlett's test, data obtained from four environments as well as pooled over the environments were subjected to the following statistical analyses at the Computer Centre, Department of Statistics, CCS HAU, Hisar.

3.5.1 Analysis of variance and co-variance:

The analysis of variance for randomized block design was carried out for individual characters for different environments to test the significance of difference among the genotypes following the method as suggested by Panse and Sukhatme (1978) (Table 4).

Model $X_{ij} = \mu + g_i + b_j + e_{ij}$

where, X_{ij}= Observation in the i^{th} treatment in the j^{th} block
μ = General mean
g_i = i^{th} genotype effect
b_j = j^{th} block effect
e_{ij} = Random error associated with i^{th} genotype in j^{th} block

The assumptions of the model are:

1. All the observations are independent.
2. The variance effects in the model are additive.
3. Error involved in the population is normally and independently distributed with mean zero and variance σ^2_e.

Table 4: Analysis of variance

Source	d.f.	Mean sum of square	Expectation of mean square	F
Replications	(r-1)	MSr		
Genotypes	(g-1)	MSg	$\sigma^2_e + \sigma^2_g$	MSg/MSe
Error	(r-1) (g-1)	MSe	σ^2_e	
Total	(n-1)			

where, r = number of replications/blocks
g = number of genotypes
σ^2_e = error variance
σ^2_g = genotypic variance

MSr, MSg and MSe stand for the mean squares due to replications, genotypes and error, respectively.

Analysis of co-variance was carried out for all the possible combination of characters as presented in Table 5.

Table 5: Analysis of co-variance

Source	d.f.	Mean sum of products	Expectation of mean square
Replications	(r-1)	MSPR	
Genotypes	(g-1)	MSPG	$\sigma_{e_{1.2}} + \sigma_{g_{1.2}}$
Error	(r-1) (g-1)	MSPE	$\sigma_{e_{1.2}}$

where, MSPR, MSPG and MSPE are the mean sum of products due to replications, genotypes and error, respectively.

3.5.2 Components of variability:

Mean: The mean value of each character was worked out by dividing the total of corresponding number of observations under all the environments.

$$\bar{X} = \frac{\Sigma X_{ij}}{N}$$

where, X_{ij} = any observation in i^{th} genotype and j^{th} replication.
N = number of observations.

Range: Lowest and highest values for each character were recorded.

Standard error: Standard error of mean was calculated with the help of error mean square from the analysis of variance (Table 4).

$$S.E. = \sqrt{\frac{2\sigma^2_e}{r}}$$

where, σ^2_e = error variance
r = number of replications

Critical difference (CD): Critical difference was calculated to compare the treatment means for all the characters using the formula given below:

$$C.D. = \sqrt{\frac{2\sigma^2_e}{r}} \quad \text{x 't' tab. at error d.f.}$$

Coefficient of variation: Coefficient of variation was estimated by the following formula:

$$CV\ (\%) = \sqrt{\frac{\sigma^2_e}{\bar{X}}} \quad \text{x 100}$$

where, σ^2_e = error variance
$\bar{X}$ = mean

Genotypic coefficient of variation:

$$GCV = \sqrt{\frac{\sigma^2_g}{\bar{X}}} \times 100$$

where,

$$\sigma^2_g = \frac{MSv - MSe}{r}$$

MSv = genotypic variance
MSe = error variance
r = number of replications
$\bar{X}$ = mean

Phenotypic coefficient of variation:

$$PCV = \sqrt{\frac{\sigma^2_p}{\bar{X}}} \times 100$$

where, $\sigma^2_p = \sigma^2_g + \sigma^2_e$
σ^2_g = genotypic variance
σ^2_e = error variance
$\bar{X}$ = mean

Heritability (Broad sense): It is the ratio of genotypic variance to the phenotypic variance. Heritability in broad sense for each character was calculated according to the following formula:

$$h^2_{(bs)\,(\%)} = \sqrt{\frac{\sigma^2_g}{\sigma^2_p}} \times 100$$

where, $h^2_{(bs)}$= Heritability broad sense
σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance

Expected genetic advance: Genetic advance as percent of mean was estimated by the formula suggested by Johnson *et al.* (1955).

$$\text{Expected genetic advance (\% of mean)} = \frac{K.\sigma^2_p.h^2}{\bar{X}} \times 100$$

where, K = selection intensity (K= 2.06)
σ^2_p = phenotypic variance
h^2 = heritability broad sense
$\bar{X}$ = mean

3.5.3 D^2 analysis (Multivariate analysis of Mahalanobis, 1936):

Following the analysis of variance and co-variance, the data were subjected to multivariate analysis. The original inter-related variables (X's) were first transformed into a set of mutually uncorrelated variables (Y's as linear function of X's) and then D^2 values were worked out. Pivotal condensation method was used to compute inverse matrix of the error dispersion matrix (Rao, 1952). The generalized distance function (D^2) between two genotypes is simply the sum of squares of differences in Y's, i.e.

$$D^2_{1.2} = \sum_{i=1}^{P} (Y_{1i} - Y_{2i})^2$$

The value between the variables on the basis of P characters is:

$$D^2_p = \sum_{i=1}^{P} \sum_{j=1}^{P} (W_{ij}) d_i d_j$$

where,

D^2_p = is the D^2 value between the variables on the basis of P characters

W_{ij} = is the inverse matrix of the pooled common dispersion obtained from error matrix.

'd' = is the difference in mean value for the characters of respective genotypes as indicated by i and j.

In brief, the estimation of D^2 values involved the following steps:

1. Pivotal condensation of error variance and covariance matrix to obtain inverse matrix.
2. Transformation of original correlated data into uncorrelated variables.
3. Calculation of mean values of the transformed characters.
4. **Calculation of D^2 values**: D^2 values between any two populations were calculated as the sum of squares of differences in the value between pairs of corresponding mean values of the transformed characters. Thus, a total of n (n-1)/2 possible combination among 50 values of D^2 were computed and arranged in the form of matrix.
5. **Determination of group constellations**: The criterion appears to be that any two genotypes belonging to the same cluster should at least, on the average, show a smaller D^2 values than those belonging to two different clusters. The D^2 values for all the combinations, presented in the matrix form were arranged in increasing order of magnitude and clustering was done according to the Tocher method suggested by Rao (1952). At first, two most closely associated genotypes were chosen and then a third genotype was located which had the smallest average D^2 values with the first two genotypes. Similarly, the fourth genotype was chosen to have the smallest average D^2 value from the first three genotypes and change in D^2 value within a cluster due to inclusion of additional genotype was computed and so on. The new genotypes were added so long the increase in average D^2 value became higher than an arbitrary value fixed then this genotype was not included in the former group. The genotypes of first cluster were omitted and rests were treated similarly for constructing new clusters.

6. **Average intra and inter-cluster distances**: The intra and inter-cluster D^2 value was calculated as under:

$$\text{Average intra-cluster distance} = \sum_{i=1}^{N} Di^2/N$$

where, Di^2 = Distance between two genotypes of i^{th} combination
N = N′(n-1)/2, n denotes number of genotypes and
N′ denotes number of combination

$$\text{Average inter-cluster distance } (i_n \rightarrow j_m) = \frac{\Sigma\, Di^2{}_{n \rightarrow m}}{nm}$$

where, i_n denotes i^{th} combination accommodating $_n$ genotypes
j_m denotes j^{th} combination accommodating $_m$ genotypes

7. **Cluster mean values**: The cluster mean for a particular character is the summation of mean values of genotypes included in a cluster, divided by number of genotypes in the same cluster. The values were calculated separately for each cluster and each character.

3.5.4 Correlation and path coefficient analysis:

Correlation coefficients: Phenotypic and genotypic correlation coefficients were worked out using variance and co-variance matrix as suggested by Robinson *et al.* (1951).

$$r\,(X_1\, X_2) = \frac{\text{Cov.}\,(X_1\, X_2)}{\sqrt{V(X_1)\, V(X_2)}}$$

where, $r\,(X_1\, X_2)$ = Correlation between X_1 and X_2
$\text{Cov.}\,(X_1\, X_2)$ = Co-variance between X_1 and X_2
$V(X_1)$ = Variance of X_1
$V(X_2)$ = Variance of X_2

Phenotypic correlations were tested at 5 per cent and 1 per cent level of significance against the Fisher's table value at (n-2) d.f.

Path-coefficient analysis: The genotypic correlation coefficients were used to work out path-coefficient analysis. Path coefficients were obtained according to Dewey and Lu (1959). A set of simultaneous equations in the following form were solved:

$r_{ny} = p_{1y} + r_{n2}p_{2y} + r_{n3}p_{3y} + \ldots\ldots + r_{nx}p_{xy}$

where, r_{ny} = correlation coefficient of one character and yield.
p_{ny} = path-coefficient between the character and yield.
$r_{n2}, r_{n3}, .. r_{nx}$ = represent correlation coefficient of that character and each of other yield components in turn.

The following correlation matrices were prepared for estimating direct and indirect path effects:

P_{n1y} The above equation can be written in matrix form as follows:

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{3y} \\ r_{ny} \end{pmatrix} = \begin{pmatrix} 1 & r_{12}, & r_{13}\ldots & r_{1n} \\ r_{21} & 1 & r_{23}\ldots & r_{2n} \\ r_{31} & r_{32} & 1\ldots & r_{3n} \\ r_{n1} & r_{n2}\ldots\ldots & \ldots\ldots & 1 \end{pmatrix} \begin{pmatrix} p_{1y} \\ p_{2y} \\ p_{3y} \\ p_{ny} \end{pmatrix}$$

$r = B.A.$

where, $r = (r_{1y}, r_{2y}, \ldots\ldots r_{ny})$
$B = (r_{ij})$correlation matrix and $A=(p_{jy})$ vector of direct effects
$A = B^{-1}.r$

Path coefficients p_{jy} were obtained as follows:

$$p_{jy} = (B^{-1}) \times (r)$$

The indirect effects for a particular character through other characters were obtained by multiplication of direct paths and particular correlation-coefficients between these two characters, respectively.

Indirect effect= $r_{ij} \times p_{jy}$

where, i = 1....n
j = 1....n
r_{ij} = correlation between two independent characters

The residual factors, i.e., the variation in yield unaccounted for those other associated factors was calculated from the following formulae:

Residual factor (%) = $1-R^2$

where, $R^2 = p_{1y} r_{1y} + p_{2y} r_{2y} + \ldots\ldots\ldots + p_{ny} r_{ny}$

R^2, is the squared multiple correlation coefficients and is the amount of variation in yield that can be accounted for by the yield component characters.

3.5.5 Stability analysis (Perkins and Jinks, 1968a) model:

The mean values recorded for 12 characters in respect of 50 genotypes in 4 environments as well as pooled over the environments were used for stability analysis following Perkins and Jinks (1968a) model which is a combined statistical and genetical approach. The biometrical genetic model is given as under:

$Y_{ij} = m + d_i + e_j + g_{ij} + e_{ij}$

where, Y_{ij} = variety mean of i^{th} variety in the j^{th} environment.
m = grand mean over all the genotypes and environments
d_i = additive genetic effect
e_j = additive environmental effect
g_{ij} = G x E interaction effect
e_{ij} = residual error variation of i^{th} variety in j^{th} environment

All these effects are assumed to be fixed. The parameters are said to be genetic in nature. Different components may be computed as under:

$m = Y..../st$
$d_i = (Y_{i.}/s)-m$
$e_j = (Y_{.j}/t)-m$
$g_{ij} = Y_{ij}-m-d_i-e_j$

where, s = the total number of environments

t = the total number of genotypes

It is known than G x E interaction of any variety is a linear function of environmental value, that is,

$g_{ij} = b_i e_j + \delta_{ij}$

So, the model becomes

$Y_{ij} = m + d_i + (1+b_i)e_j + \delta_{ij} + e_{ij}$

where,

$$b_i = (\Sigma_j g_{ij} e_j)^2 / \Sigma_j e_j^2 \text{ and } (1+b_i) = \Sigma_j Y_{ij} e_j / \Sigma_j e_j^2$$

For each variety, the regression S.S. is obtained as:

$$(1+b_i)^2 \Sigma_j e_j^2 = (\Sigma_j Y_{ij} e_j)^2 / \Sigma_i e_j^2$$

and deviation from regression S.S. = $\Sigma_j \delta_{ij}^2$

Each mean square can be compared with the σ^2_e, the error mean square, but in order to show that regression mean square accounts for a significantly larger portion of the total variation, it should be compared with:

$$\frac{\Sigma_j \delta_{ij}^2}{(s-2)}$$

since,

$$(\Sigma_j Y_{ij} e_j)^2 / \Sigma_j e^{m2} = (1+b_i)^2 \Sigma_j e_j^2$$

For the regression mean square, it is apparent that we are testing the hypothesis that a significant portion of the variation of the j^{th} variety over environments is accounted for by fitting the regression slope of $(1+b_i)$. This, however, accounts both for additive environmental variation and that part of the G x E interaction variation which is a linear function of the environmental values. The significance of b_i was, therefore, tested as the difference between $(1+b_i)$ and 1.

The b_i values for the different lines were compared by using a joint regression analysis based on the comparison $(1+b_i)$ values which gives:

$$\Sigma_i \text{ (reg. S.S.)} = \Sigma_i (1+b_i)^2 \Sigma_i e^2_j$$

and since $\Sigma b_i = 0$, this becomes

$$= t \Sigma_i e^2_j + \Sigma_i b_i^2 \Sigma_j e^2_j$$

The joint regression S.S. is $t \Sigma_i e^2_j$ and equals in this analysis to the environmental S.S. The heterogeneity between regression S.S. is: $\Sigma_j b_i^2 \Sigma_j e^2_j$.

The expectations of mean squares in the joint regression analysis are shown in Table 6.

r, s and t indicates number of replications, environments and genotypes, respectively.

Test of significance

(a) The mean squares: Mean squares due to genotypes, environments, G x E interaction, heterogeneity between regression and remainder were tested against pooled error. If remainder is significant then mean squares due to genotypes, environments, G x E interaction and heterogeneity between regression were tested against remainder mean square.

Table 6: Analysis of variance for joint regression

Source of variation	d.f.	Sum of square	Expectation of mean square
Genotypes	(t-1)	$\Sigma_j Y^2_i/s - Y^2/st$	$s\Sigma_j(d_i)^2/(t-1)$
Environments (joint regression)	(s-1)	$\Sigma_j Y^2_{.i}/t - Y^2/st$	$t\Sigma_j(e_i)^2/(s-1)$
G x E	(t-1)(s-1)	$\Sigma_i\Sigma_j(Y^2_{ij}) - \Sigma Y_i^2/s$ or $\Sigma_i\Sigma_j(Y^2_{ij}) - \Sigma_j Y_i^2/s - \Sigma Y^2_j/t + Y^2/st$	
Heterogeneity between regression	(t-1)	$\Sigma_j [\Sigma_j Y_{ij} (Y_{.j}/t - Y../st)]^2/\Sigma_j 1^2_j$ - Env.S.S.	$\Sigma_i(b_i)^2\Sigma_j(e_j)^2/(t-1)$
Remainder	(t-1) (s-2)	By subtracting heterogeneity S.S. from Lines x Env. S.S.	$\dfrac{\Sigma_i[\Sigma_j\delta_{ij}^2]}{(t-1)(s-2)}$
Error	s (t-1) (r-1)		σ^2_e

(b) Stability parameters: The stability parameters of genotype for the evaluated characters were based on the mathematical model of

Perkins and Jinks (1968a). Test of significance for stability parameters, regression coefficient (b_i) and deviation from regression ($S^{-2}d_i$) is given as follows:

(i) Testing of regression coefficient (b_i):

For testing of individual b_i value 't' test was used as:

$$\text{'t'} = \frac{b_i}{SE(b_i)} \text{ at (t-2) degree of freedom}$$

where,

$$SE(b_i) = \sqrt{\frac{\Sigma_i \delta^2_{ij}(s-2)}{\Sigma_I{}^2_j}}$$

I_j= Environmental index

It was obtained as the mean of all the genotypes at j^{th} environment (site mean) minus grand mean, i.e., $I_j = Y_{.j}/t - Y../st$

(ii) Testing of deviation from regression ($S^{-2}d_i$)

Significance of individual $S^{-2}d_i$ was tested by 'F' test

where.

$F = [\Sigma_j \delta^2_{ij}/(s-2)]$/ Pooled error d.f.$\sigma^2_e$ at (s-2) and s (t-1) (r-1)

CHAPTER-IV

EXPERIMENTAL RESULTS

EXPERIMENTAL RESULTS

The results obtained from various experiments to fulfill the objectives have been described under the following heads:

4.1 Analysis of variance

4.2 Mean, range and components of variation

4.3 Genetic divergence

4.4 Correlation coefficients

4.5 Path-coefficient analysis

4.6 Stability analysis

4.1 ANALYSIS OF VARIANCE

The analysis of variance was carried out for 12 characters in 4 environments as well as pooled over the environments is presented in Table 7. Mean squares due to genotypes were highly significant for all the characters. This indicated that wide range of genetic variability was present among the genotypes for various traits. The coefficient of variation was low (<15%) for all the characters in all the environments.

4.2 MEAN, RANGE AND COMPONENTS OF VARIATION

The mean, range, genotypic and phenotypic coefficient of variation, heritability and genetic advance as percent of mean are presented in Table 8. Maximum mean values for all the fodder yield and quality characters were recorded in E_1 followed by E_3 and minimum in E_4. E_2 had lowest mean for days to 50 per cent flowering. However, leaf: stem ratio was at par in E_1 and E_2. Early flowering was observed in late sown environments (E_2 and E_4). Performance for different characters in timely sown environments (E_1 and E_3) was better than that of late sown environments (E_2 and E_4) as compared to pooled basis. Wide range of variation for fodder yield per plant and

Table 7: Analysis of variance for fodder yield, its components and quality characters in oats

	Sources	D.F.	Mean sum of squares											
			Days to 50% flowering	Plant height (cm)	No. of tillers/ plant	Stem diameter (mm)	No. of leaves/ plant	Leaf length (cm)	Leaf breadth (cm)	Leaf: stem ratio	Green fodder yield/plant (g)	Dry fodder yield/plant (g)	Crude protein content (%)	*In vitro* dry matter digestibility (%)
E_1	Replications	2	1.727	3.687	0.112	0.052	2.687	0.327	0.001	0.001	155.120	6.727	0.230	0.779
	Genotypes	49	84.640**	488.923**	10.092**	2.266**	384.226**	97.061**	0.297**	0.008**	23987.005**	1219.014**	1.999**	34.654**
	Error	98	0.958	2.156	0.535	0.117	8.129	1.367	0.010	0.001	325.712	13.604	0.096	3.680
	CV (%)	-	0.890	1.300	5.962	4.096	4.296	2.290	4.170	8.932	4.097	4.203	3.392	2.883
	CD at 5%	-	1.566	2.350	1.171	0.547	4.563	1.871	0.160	0.051	28.882	5.903	0.496	3.070
E_2	Replications	2	1.947	8.207	0.062	0.237	3.607	1.127	0.019	0.001	8.540	0.187	0.061	5.526
	Genotypes	49	68.681**	419.391**	7.224**	3.060**	315.106**	91.850**	0.296**	0.013**	9115.823**	369.022**	1.821**	31.343**
	Error	98	1.124	3.635	0.276	0.164	4.090	1.304	0.008	0.001	70.377	4.010	0.045	2.787
	CV (%)	-	1.240	1.885	5.315	5.183	3.774	2.381	4.010	8.833	4.021	4.715	2.416	2.594
	CD at 5%	-	1.697	3.051	0.840	0.648	3.236	1.827	0.143	0.051	13.425	3.205	0.339	2.672
E_3	Replications	2	0.787	1.007	0.023	0.049	0.740	0.887	0.016	0.002	8.427	1.287	0.021	0.682
	Genotypes	49	99.541**	582.259**	6.758**	2.291**	205.728**	93.139**	0.197**	0.007**	9137.351**	422.846**	1.928**	43.069**
	Error	98	0.746	3.803	0.225	0.091	4.284	1.574	0.009	0.001	131.297	5.933	0.108	3.475
	CV (%)	-	0.705	1.695	6.052	3.633	4.791	2.581	4.032	10.436	4.434	4.641	3.626	2.828
	CD at 5%	-	1.382	3.121	0.760	0.483	3.312	2.008	0.152	0.051	18.337	3.898	0.526	2.983
E_4	Replications	2	1.147	3.500	0.085	0.218	2.407	0.447	0.002	0.001	70.907	4.347	0.353	7.272
	Genotypes	49	48.575**	439.456**	13.086**	3.290**	364.629**	54.422**	0.201**	0.014**	4739.903**	168.339**	1.330**	33.782**
	Error	98	0.841	4.112	0.271	0.126	4.604	1.277	0.009	0.002	46.703	2.768	0.067	3.558
	CV (%)	-	0.850	2.020	6.274	4.850	4.702	2.460	4.510	13.429	4.290	5.061	3.038	3.033
	CD at 5%	-	1.468	3.245	0.833	0.568	3.434	1.808	0.152	0.072	10.937	2.663	0.414	3.018
P	Replications	2	1.205	3.912	0.201	0.010	1.699	3.021	0.009	0.001	12.280	6.586	0.074	6.388
	Genotypes	49	36.726**	386.006**	6.703**	1.924**	224.809**	63.726**	0.203**	0.007**	7219.156**	333.089**	1.526**	30.838**
	Error	98	0.260	0.864	0.131	0.040	1.798	0.951	0.007	0.001	42.385	2.431	0.027	1.167
	CV (%)	-	0.480	0.870	3.782	2.520	2.569	2.015	3.682	9.355	2.441	2.893	1.852	1.668
	CD at 5%	-	0.816	1.488	0.579	0.320	2.146	1.561	0.134	0.050	10.419	2.495	0.263	1.729

**Significant at P=0.01; P=Pooled analysis

Table 8: Mean, range, coefficient of variation, heritability and genetic advance for fodder yield, its components and quality traits in oats

Characters		Mean	Range	GCV	PCV	Heritability (broad sense)	Genetic advance (% of mean)
Days to 50% flowering	E_1	110.42	96.00-125.00	4.78	4.86	96.68	9.68
	E_2	85.53	74.00-93.33	5.54	5.68	95.24	11.15
	E_3	122.58	110.00-131.00	4.68	4.73	97.78	9.53
	E_4	107.96	97.66-120.67	3.69	3.79	94.98	7.41
	P	106.62	98.75-113.16	3.26	3.30	97.90	6.66
Plant height (cm)	E_1	113.03	91.67-140.33	11.27	11.34	98.68	23.06
	E_2	101.16	74.00-124.67	11.63	11.78	97.44	23.66
	E_3	115.06	89.00-145.67	12.06	12.18	98.06	24.61
	E_4	100.37	68.70-126.33	12.00	12.17	97.24	24.37
	P	107.41	84.16-133.41	10.54	10.58	99.33	21.65
No. of tillers/plant	E_1	12.26	9.30-16.50	14.54	15.72	85.61	27.73
	E_2	9.88	6.80-15.00	15.39	16.29	89.33	29.98
	E_3	7.83	4.60-11.87	18.83	19.77	90.63	36.92
	E_4	8.29	4.60-13.40	24.91	25.68	94.03	49.76
	P	9.57	6.85-13.31	15.48	15.94	94.36	30.99
Stem diameter (mm)	E_1	8.35	5.67-9.90	10.13	10.93	85.97	19.36
	E_2	7.81	5.57-9.87	12.57	13.60	85.46	23.94
	E_3	8.30	6.10-9.90	10.31	10.93	88.99	20.04
	E_4	7.32	4.40-9.33	14.02	14.84	89.29	27.30
	P	7.95	5.77-9.74	9.95	10.27	94.00	19.89
No. of leaves/plant	E_1	66.37	43.33-91.33	16.86	17.40	93.91	33.67
	E_2	53.59	38.00-92.67	18.99	19.37	96.20	38.38
	E_3	43.19	25.67-66.33	18.96	19.56	94.00	37.88
	E_4	45.63	28.00-76.67	24.00	24.46	96.30	48.53
	P	52.20	36.83-78.75	16.49	16.69	97.63	33.58
Leaf length (cm)	E_1	51.04	34.67-62.67	11.06	11.29	95.88	22.31
	E_2	47.95	34.00-56.66	11.45	11.70	95.86	23.10
	E_3	48.60	34.33-58.67	11.36	11.65	95.09	22.83
	E_4	45.95	32.33-53.00	9.15	9.48	93.27	18.22
	P	48.39	34.25-55.41	9.45	9.66	95.65	19.04

Continue.

Characters		Mean	Range	GCV	PCV	Heritability (broad sense)	Genetic advance (% of mean)
Leaf breadth (cm)	E_1	2.39	1.83-3.03	12.90	13.57	90.32	25.26
	E_2	2.23	1.73-2.97	13.90	14.47	92.27	27.52
	E_3	2.35	1.90-2.97	10.62	11.40	86.86	20.40
	E_4	2.10	1.50-2.87	12.01	12.79	88.08	23.22
	P	2.27	1.78-2.91	11.21	11.80	90.10	21.92
Leaf: stem ratio	E_1	0.35	0.26-0.47	14.44	15.73	84.28	27.31
	E_2	0.35	0.23-0.61	17.63	19.09	85.30	33.55
	E_3	0.30	0.23-0.43	15.07	16.27	85.73	28.74
	E_4	0.33	0.22-0.52	20.04	20.43	96.21	40.50
	P	0.33	0.27-0.50	14.32	14.63	95.82	28.89
Green fodder yield/plant (g)	E_1	440.46	210.00-598.67	20.16	20.57	96.03	40.70
	E_2	208.62	107.67-328.33	26.32	26.62	97.71	53.59
	E_3	258.40	163.67-398.67	21.20	21.66	95.80	42.75
	E_4	159.30	74.33-264.33	24.82	25.19	97.10	50.39
	P	266.69	175.50-375.17	18.33	18.49	98.25	37.44
Dry fodder yield/plant (g)	E_1	87.74	40.00-131.67	22.84	23.22	96.72	46.28
	E_2	42.47	20.67-69.00	25.97	26.39	96.81	52.63
	E_3	52.48	35.33-85.00	22.46	22.93	95.90	45.31
	E_4	32.87	16.67-49.67	22.59	23.15	95.22	45.42
	P	53.89	34.58-79.00	19.46	19.68	97.84	39.66
Crude protein content (%)	E_1	9.13	7.63-11.40	8.72	9.35	86.84	16.74
	E_2	8.77	7.60-11.80	8.76	9.09	92.88	17.39
	E_3	9.06	7.50-11.30	8.59	9.32	84.88	16.31
	E_4	8.51	7.20-10.13	7.61	8.19	86.35	14.58
	P	8.87	7.77-11.11	7.95	8.16	94.96	15.97
In vitro dry matter digestibility (%)	E_1	66.54	59.87-74.07	4.82	5.62	73.73	8.54
	E_2	64.36	58.90-70.67	4.79	5.45	77.33	8.68
	E_3	65.91	59.76-73.43	5.51	6.19	79.14	10.09
	E_4	62.19	54.47-69.00	5.10	5.93	73.90	9.03
	P	64.75	58.46-71.22	4.85	5.13	89.44	9.46

GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation; P=Pooled analysis

most of the traits was observed in E_1 followed by E_3 (Appendix-I-VI)

Genotypic and phenotypic coefficient of variation was highest for green and dry fodder yield per plant followed by leaves and tillers per plant in all the environments. Both of these parameters were quite close to each other for different characters. The magnitude of genotypic coefficient of variation was considerably reduced in comparison to phenotypic coefficient of variation in pooled analysis.

The estimates of heritability in broad sense ranged from 73.73 to 98.68 per cent in E_1 , 77.33 to 97.71 per cent in E_2 , 79.14 to 98.06 per cent in E_3 and 73.90 to 97.24 per cent in E_4, whereas it ranged from 89.44 to 99.33 per cent in pooled analysis. The estimates of heritability were high for all the traits in all the environments except for IVDMD.

The genetic advance as percent of mean varied from 8.54 to 46.28 in E_1, 8.68 to 53.59 in E_2, 9.53 to 45.31 in E_3 and 7.41 to 50.39 in E_4 and in pooled analysis, it varied from 6.66 to 39.66. High genetic advance was observed for all the traits. Days to 50 per cent flowering and IVDMD had low genetic advance in all environments as well as in pooled analysis, whereas it was moderate for crude protein content in all the environments.

High heritability coupled with high genetic advance was observed for plant height, tillers per plant, stem diameter, number of leaves per plant, leaf length, leaf breadth, leaf: stem ratio, green and dry fodder yield per plant in all the environments, whereas days to 50 per cent flowering had high estimates of heritability and low genetic advance. However, crude protein content was having high heritability with moderate genetic advance.

4.3 GENETIC DIVERGENCE

Since the analysis of variance revealed significant differences for all the characters studied, therefore, the analysis was extended for estimating D^2 values. Fifty genotypes were grouped into 8 clusters in

E_1 and E_2 and 9 clusters in E_3 and E_4 but in pooled analysis 10 clusters were formed. The clustering pattern obtained in the present study revealed that genetic diversity was not always related with geographical diversity. The composition of different clusters varied, containing 1 to 13 genotypes in E_1, 1 to 14 in E_2 and E_3, 1 to 16 in E_4 and 1 to 11 in pooled analysis in most of the clusters involving strains from different areas and sources. Similarly, the strains developed at one station were also grouped in different clusters (Table 9).

Out of 8 clusters in E_1, cluster I was the largest comprising 13 genotypes followed by cluster II consisting of 8 genotypes; cluster III and IV with 7 genotypes, cluster V, VI, VII and VIII contained 6, 4, 4 and 1 genotypes, respectively, however these were solitary in regard to multivariate composition.

In E_2, cluster I had the largest number, i.e., 14 genotypes, followed by cluster II comprising 12 genotypes and cluster III containing 6 genotypes, cluster IV and V, which contained 5 genotypes each. Clusters VI, VII and VIII had 4, 3 and 1 genotypes, respectively.

Maximum number of genotypes (14) were included in cluster I of E_3, while clusters II, III and IV had 8, 7 and 6 genotypes, respectively. Cluster V, VI and VII each had 4 genotypes, cluster VIII contained 2 genotypes and IX had one genotype only.

Genotypes in E_4 were grouped in 9 clusters, cluster I was the largest having 16 genotypes, followed by cluster II which had 9 genotypes. Clusters III and IV; V and VI; VII and VIII had 5, 4 and 3 genotypes, respectively, and cluster IX included one genotype only.

In pooled analysis 10 clusters were formed. Out of 10 clusters, 11 genotypes were included in cluster I followed by cluster II which had 10 genotypes, while clusters III, IV, V and VI comprised of 7, 6, 5,4 genotypes, respectively. Cluster VII, VIII and IX contained 2 genotypes each. The smallest cluster X had only one genotype.

Table 9: Clustering pattern of 50 genotypes of oats in different environments

Cluster		No. of genotypes	Genotypes
I	E_1	13	Kent, HJ-8, HFO-114, JHO-95-2, JHO-96-4, JHO-96-6, JHO-866, DFO-54, OL-805, OS-6, OS-7, OS-174, OS-237
	E_2	14	JHO-889, JHO-897, JHO-995, JHO-99-3, JHO-99-4, JHO-99-5, DFO-57, S-2688, S-3021, OS-245, OS-277, OS-279, OS-285, OS-286
	E_3	14	HJ-8, JHO-810, JHO-822, JHO-866, JHO-851E, JHO-99-1, JHO-99-2, JHO-99-6, Blacknip, JHO-99-7, UPO-212, UPO-248, OS-285, OS-286
	E_4	16	JHO-97-4, JHO-810, JHO-851, JHO-866, JHO-851 E, JHO-99-6, JHO-99-7, UPO-248, S-2688, OS-7, OS-174, OS-189, OS-237, OS-242, OS-285, OS-286
	P	11	JHO-97-4, JHO-810, JHO-822, JHO-99-7, UPO-250, DFO-57, OL-661, OL-805, OL-936, OS-6, OS-7
II	E_1	8	JHO-99-6,, Blacknip, JHO-99-7, UPO-212, UPO-230, UPO-248, S-3021, OS-189
	E_2	12	Kent, JHO-96-4, JHO-96-6, JHO-851, JHO-851E, JHO-99-1, JHO-99-2, JHO-99-6, Blacknip, JHO-99-7, UPO-250, UPO-288
	E_3	8	Kent, HFO-114, JHO-95-2, JHO-96-4, JHO-96-6, UPO-250, UPO-288, DFO-54
	E_4	9	JHO-94-1, JHO-94-3, JHO-95-1, JHO-99-3, JHO-99-4, JHO-99-5, OS-245, OS-277, OS-279
	P	10	Kent, HJ-8, HFO-114, JHO-95-2, JHO-96-4, JHO-96-6, JHO-851E, JHO-99-1, JHO-99-2, OS-174.
III	E_1	7	JHO-97-4, JHO-810, JHO-822, JHO-851E, JHO-99-1, JHO-99-2, S-2688
	E_2	6	UPO-230, OL-805, OL-936, OS-6, OS-7, OS-174
	E_3	7	JHO-94-3, DFO-57, S-2688, S-3021, OS-245, OS-277, OS-279
	E_4	5	JHO-822, JHO-897, JHO-995, DFO-57, S-3021
	P	7	JHO-94-1, JHO-94-3, JHO-829, JHO-866, JHO-889, JHO-897, JHO-995
IV	E_1	7	JHO-897, JHO-995, JHO-99-3, JHO-99-4, JHO-99-5, OS-285, OS-286
	E_2	5	JHO-829, JHO-866, UPO-212, UPO-248, OS-242
	E_3	6	JHO-829, JHO-851, JHO-995, OS-189, OS-237, OS-242
	E_4	5	Kent, HJ-8, HFO-114, JHO-95-2, JHO-96-4
	P	6	Blacknip, UPO-212, UPO-230, UPO-248, OS-189, OS-237
V	E_1	6	JHO-94-1, JHO-94-3, JHO-95-1, OS-245, OS-277, OS-279
	E_2	5	JHO-97-4, JHO-810, JHO-822, DFO-54, OL-661
	E_3	4	JHO-94-1, JHO-99-3, JHO-99-4, JHO-99-5
	E_4	4	JHO-96-6, JHO-829, UPO-212, UPO-230
	P	5	JHO-851, JHO-99-3, JHO-99-5, OS-277, OS-279

Continue..

Cluster		No. of genotypes	Genotypes
VI	E_1	4	JHO-829, JHO-851, JHO-889, OS-242
	E_2	4	HJ-8, HFO-114, OS-189, OS-237
	E_3	4	UPO-230, OS-6, OS-7, OS-174
	E_4	4	UPO-250, UPO-288, DFO-54, OS-6
	P	4	JHO-99-6, S-2688, S-3021, OS-242
VII	E_1	4	UPO-250, UPO-288, OL-661, OL-936
	E_2	3	JHO-94-1, JHO-94-3, JHO-95-1
	E_3	4	JHO-97-4, OL-661, OL-805, OL-936
	E_4	3	JHO-889, JHO-99-1, JHO-99-2
	P	2	JHO-99-4, OS-245
VIII	E_1	1	DFO-57
	E_2	1	JHO-95-2
	E_3	2	JHO-889, JHO-897
	E_4	3	OL-661, OL-805, OL-936
	P	2	OS-285, OS-286
IX	E_1	-	-
	E_2	-	-
	E_3	1	JHO-95-1
	E_4	1	Blacknip
	P	2	UPO-288, DFO-54
X	E_1	-	-
	E_2	-	-
	E_3	-	-
	E_4	-	-
	P	1	JHO-95-1

P= Pooled analysis

The average intra and inter-cluster distances are presented in Table 10. The intra-cluster distances were relatively smaller than inter-cluster distances indicating homogenous nature of the groups and presence of narrow genetic variation within a cluster in all the environments. The intra-cluster D^2 values varied from 0.0 (VIII) to 34.50 (VI). The inter-cluster divergence ranged from 55.00 (II and VIII) to 1014.81 (III and V) in E_1.

In E_2, the computed D^2 values varied appreciably from 40.20 (IV and VIII) to 998.65 (V and VII) showing high divergence among different genotypes. The intra-cluster distance ranged from 0.0 (VIII) to 35.40 (III) which had 6 genotypes, whereas in E_3, the inter cluster distances revealed that the maximum divergent clusters were V and VII (6060.81), followed by cluster VII and IX (5682.50) and III and VII (5240.07). The divergence was minimum (194.78) between the clusters I and VI. However, intra-cluster D^2 values varied from 0.0 (IX) to 99.37 (III).

The inter-cluster distances in E_4 indicated that the most diverse genotypes were in clusters II and IV (9938.09), IV and VIII (6268.00) and II and VI (5018.36). However, in E_4 intra-cluster distance ranged from 0.0 (IX) to 99.20 (IV).

Based on pooled D^2 analysis, the average intra-cluster values varied from 0.0 (X) to 24.70 (I), whereas inter-cluster values ranged between 43.08 (IV and VI) to 1846.50 (IX and X) indicating considerable diversity between the clusters. In general, cluster X was found to be situated maximum apart from all the other clusters.

The cluster mean estimated over the genotypes included in a cluster for 12 characters in different environments is presented in Table 11. In E_1, cluster II possessed high mean values for days to 50 per cent flowering (112.46), plant height (118.08), stem diameter (9.00), leaf breadth (2.55), crude protein content (9.78) and IVDMD (70.56); cluster VIII for number of tillers per plant (14.13), leaf

Table 10: Average intra and inter-cluster D^2 values among 50 genotypes of oats in different environments

Cluster		I	II	III	IV	V	VI	VII	VIII	IX	X
I	E_1	33.08	131.34	191.29	143.24	489.44	79.58	78.23	311.92	-	-
	E_2	31.17	193.49	183.39	280.51	426.81	293.39	146.83	138.77	-	-
	E_3	88.70	308.35	3371.87	533.09	4005.56	194.78	221.23	585.32	3665.50	-
	E_4	86.28	2982.85	318.47	1657.30	300.72	588.45	540.72	1413.95	465.81	-
	P	24.70	124.54	581.65	62.15	503.04	100.16	350.04	137.86	63.64	1247.54
II	E_1		27.67	239.63	159.93	314.79	120.66	249.00	55.00	-	-
	E_2		32.07	62.60	57.03	71.64	46.22	630.71	40.58	-	-
	E_3		98.98	3521.59	847.44	4244.75	443.31	365.97	918.37	4253.25	-
	E_4		69.19	1323.00	9938.09	4783.11	5018.36	2482.37	347.96	4600.00	-
	P		19.78	279.56	184.63	216.20	328.67	285.15	119.45	105.40	698.00
III	E_1			21.70	492.26	1014.81	274.46	90.68	106.14	-	-
	E_2			35.40	81.18	68.67	60.34	680.83	71.33	-	-
	E_3			99.37	1286.52	249.61	3992.98	5240.07	1031.78	475.86	-
	E_4			99.10	3101.68	758.15	1145.05	303.60	548.80	318.40	-
	P			23.04	442.55	108.46	392.54	238.14	191.00	966.78	74.28
IV	E_1				33.73	177.28	82.00	460.14	151.00	-	-
	E_2				35.10	135.60	46.15	814.60	40.20	-	-
	E_3				98.33	1585.33	568.00	1446.79	244.42	1335.16	-
	E_4				99.20	835.20	774.75	2490.60	6268.00	889.60	-
	P				19.80	461.07	43.08	365.08	106.08	66.75	1177.67
V	E_1					25.53	354.58	991.16	128.00	-	-
	E_2					34.00	88.10	998.65	69.20	-	-
	E_3					96.50	4756.75	6060.81	1441.50	212.00	-
	E_4					48.50	318.12	627.83	2527.50	357.00	-
	P					24.11	288.80	64.50	139.40	898.80	176.00

Continue..

Cluster		I	II	III	IV	V	VI	VII	VIII	IX	X
VI	E_1						34.50	197.00	218.50	-	-
	E_2						26.67	833.33	78.75	-	-
	E_3						43.47	446.00	991.38	4492.50	-
	E_4						96.00	726.83	2910.33	668.00	-
	P						23.84	192.25	105.25	106.13	818.00
VII	E_1							23.33	260.25	-	-
	E_2							12.30	493.00	-	-
	E_3							42.67	1516.25	5682.50	-
	E_4							49.67	829.33	230.33	-
	P							24.00	84.50	715.00	172.00
VIII	E_1								00.00	-	-
	E_2								00.00	-	-
	E_3								2.00	1371.50	-
	E_4								47.67	1781.66	-
	P								10.00	346.00	587.50
IX	E_1									-	-
	E_2									-	-
	E_3									00.00	-
	E_4									00.00	-
	P									4.41	1846.50
X	E_1										-
	E_2										-
	E_3										-
	E_4										-
	P										00.00

P= Pooled analysis

Table 11: Cluster mean values for fodder yield, its components and quality traits of oats in different environments

Cluster		Days to 50% flowering	Plant height (cm)	No. of tillers/ plant	Stem diameter (mm)	No. of leaves/ plant	Leaf length (cm)	Leaf breadth (cm)	Leaf: stem ratio	Green fodder yield/ plant (g)	Dry fodder yield/ plant (g)	Crude protein content (%)	*In vitro* dry matter digestibility (%)
I	E_1	109.31	114.41	12.12	8.55	64.95	52.92	2.39	0.34	428.54	85.13	9.00	66.68
	E_2	87.65	102.79	9.46	8.05	50.93	47.61	2.24	0.35	204.94	43.76	8.59	62.73
	E_3	121.26	112.00	8.22	8.46	45.38	48.50	2.41	0.32	262.83	51.19	9.63	67.07
	E_4	108.84	103.49	8.82	6.79	48.98	45.98	2.13	0.35	165.36	33.28	8.57	62.10
	P	105.70	102.97	10.13	7.68	54.89	49.12	2.19	0.34	269.21	54.44	8.79	63.61
II	E_1	112.46	118.08	11.63	9.00	68.54	52.37	2.55	0.39	483.25	94.33	9.78	70.56
	E_2	88.44	97.54	10.59	7.66	61.18	46.48	2.04	0.40	203.36	40.15	8.93	64.24
	E_3	107.00	107.17	8.14	8.49	43.29	48.50	2.31	0.29	263.59	50.04	8.77	66.62
	E_4	107.52	102.79	7.19	7.14	37.70	45.18	2.03	0.28	145.47	30.72	8.31	60.74
	P	106.37	107.10	10.20	7.88	55.45	48.73	2.24	0.34	265.93	51.66	8.82	64.98
III	E_1	112.14	103.71	14.00	7.89	72.71	47.00	2.21	0.36	437.47	85.81	8.93	66.33
	E_2	87.05	105.28	9.18	7.90	47.85	49.95	2.33	0.34	226.32	46.62	8.48	63.26
	E_3	123.24	115.24	7.27	8.18	39.29	51.62	2.32	0.32	243.24	50.43	8.49	63.87
	E_4	107.74	90.60	8.56	7.42	45.46	46.52	2.08	0.34	141.56	31.06	8.54	62.76
	P	107.30	103.97	10.21	7.86	54.30	46.04	2.24	0.31	265.95	51.99	9.42	66.30
IV	E_1	112.00	112.24	11.98	8.24	65.52	51.72	2.49	0.35	453.57	90.62	9.18	64.42
	E_2	84.58	99.74	10.16	8.18	55.12	46.46	2.28	0.33	216.48	43.24	9.24	66.68
	E_3	125.33	128.61	8.43	8.48	46.11	46.83	2.43	0.29	286.50	62.40	8.74	65.83
	E_4	107.74	102.60	8.48	7.30	46.00	48.52	2.20	0.34	177.54	35.68	8.56	65.66
	P	108.10	114.53	8.24	8.78	48.60	49.50	2.51	0.35	291.00	59.72	9.51	67.48
V	E_1	107.28	113.00	10.72	8.06	54.11	49.45	2.45	0.35	362.17	75.00	8.85	66.12
	E_2	80.38	91.68	10.20	6.94	51.04	47.94	2.00	0.36	169.22	33.00	8.70	64.44
	E_3	121.58	114.17	7.10	7.69	37.25	45.25	2.18	0.29	192.01	42.60	9.31	62.76
	E_4	107.03	99.65	9.13	7.10	40.15	44.00	2.03	0.33	165.50	33.65	8.98	64.65
	P	106.72	106.32	9.77	7.42	52.24	48.40	2.18	0.35	234.98	50.40	8.45	61.26

Continue...

Cluster		Days to 50% flowering	Plant height (cm)	No. of tillers/ plant	Stem diameter (mm)	No. of leaves/ plant	Leaf length (cm)	Leaf breadth (cm)	Leaf: stem ratio	Green fodder yield/ plant (g)	Dry fodder yield/ plant (g)	Crude protein content (%)	*In vitro* dry matter digestibility (%)
VI	E_1	109.83	114.75	13.53	7.96	75.33	47.83	2.36	0.34	443.58	91.50	9.19	65.26
	E_2	85.40	114.75	9.95	9.05	55.90	53.07	2.78	0.34	272.10	52.65	8.93	65.93
	E_3	121.00	119.00	6.75	8.43	38.17	46.58	2.41	0.28	250.59	56.33	8.88	65.67
	E_4	101.85	105.18	6.88	7.28	37.15	47.10	2.13	0.28	146.98	32.65	8.18	61.65
	P	109.15	110.33	9.69	8.18	53.55	50.13	2.38	0.37	292.63	58.35	8.44	65.92
VII	E_1	111.08	117.08	12.14	8.41	65.33	52.33	2.27	0.29	467.26	94.84	8.97	64.70
	E_2	86.33	100.76	9.43	6.96	47.67	45.20	2.20	0.31	188.10	39.76	9.03	67.96
	E_3	126.67	115.67	7.93	7.81	45.58	53.24	2.18	0.31	260.83	52.83	8.96	65.10
	E_4	109.43	103.87	9.73	8.37	57.20	45.33	2.20	0.35	210.20	40.90	8.83	60.87
	P	107.55	117.85	6.98	8.55	38.45	50.20	2.50	0.32	241.15	52.50	8.49	61.00
VIII	E_1	104.33	102.33	14.13	7.73	71.00	57.00	2.20	0.44	532.34	95.67	8.87	63.97
	E_2	88.00	98.67	9.73	5.97	48.67	53.67	1.73	0.39	182.33	34.67	8.27	66.13
	E_3	127.34	110.34	7.95	8.64	49.17	44.84	2.49	0.28	308.34	57.00	9.39	69.05
	E_4	109.40	101.10	8.70	7.00	50.77	46.90	1.93	0.38	153.80	31.90	8.17	59.87
	P	106.00	104.95	8.15	7.70	45.70	51.65	2.34	0.34	236.70	48.15	8.79	61.20
IX	E_1	-	-	-	-	-	-	-	-	-	-	-	-
	E_2	-	-	-	-	-	-	-	-	-	-	-	-
	E_3	127.67	127.67	7.13	8.20	39.33	51.00	2.50	0.27	280.00	59.00	9.10	70.10
	E_4	120.67	68.70	4.60	8.70	28.00	38.33	2.43	0.52	74.33	16.67	9.93	67.50
	P	99.35	107.00	9.04	8.15	45.85	48.65	2.25	0.29	262.85	56.30	8.55	63.45
X	E_1	-	-	-	-	-	-	-	-	-	-	-	-
	E_2	-	-	-	-	-	-	-	-	-	-	-	-
	E_3	-	-	-	-	-	-	-	-	-	-	-	-
	E_4	-	-	-	-	-	-	-	-	-	-	-	-
	P	110.67	121.50	8.60	8.22	47.50	49.50	2.49	0.31	283.17	60.33	8.81	68.28

P = Pooled analysis

length (57.00), leaf: stem ratio (0.44), green and dry fodder yield per plant (532.34, 95.67, respectively) and cluster VI for number of leaves per plant (75.33). On the other hand, cluster V had lowest means for green and dry fodder yield per plant (362.17, 75.00, respectively).

Cluster VI had highest mean values for plant height (114.75), stem diameter (9.05), leaf breadth (2.78), green and dry fodder yield per plant (272.10, 52.65, respectively); cluster II for days to 50 per cent flowering (88.44), number of tillers (10.59) and leaves per plant (61.18) and leaf: stem ratio (0.40); cluster VIII for leaf length (53.67); cluster IV for crude protein content (9.24) and cluster VII for IVDMD (67.96), whereas cluster V had lowest green and dry fodder yield per plant in E_2.

Mean of cluster IV in E_3 was maximum for plant height (128.61), number of tillers per plant (8.43) and dry fodder yield per plant (62.40); cluster I for leaf: stem ratio (0.32) and crude protein content (9.63); cluster IX for days to 50 per cent flowering (127.67), leaf breadth (2.50) and IVDMD (70.10); cluster VIII for stem diameter (8.64), number of leaves per plant (49.17) and green fodder yield per plant (308.34); cluster VII for leaf length (53.24), whereas cluster V had minimum mean for most of the traits except for days to 50 per cent flowering and plant height.

Cluster IX possessed high mean values for days to 50 per cent flowering (120.67), stem diameter (8.70), leaf breadth (2.43), leaf: stem ratio (0.52), crude protein content (9.93) and IVDMD (67.50). Cluster VII had high mean values for number of tillers (9.73) and leaves per plant (57.20), green and dry fodder yield per plant (210.20, 40.90, respectively) and cluster IV and VI had high mean values only for leaf length (48.52) and plant height (105.18), respectively indicating considerable cluster means for all the characters in E_4.

The cluster means estimated over the genotypes in pooled analysis for all the characters revealed considerable inter-cluster variation. Cluster X had maximum mean values for days to 50 per cent flowering (110.67), plant height (121.50), dry fodder yield per plant (60.33) and IVDMD (68.28), cluster IV for stem diameter (8.78), leaf breadth (2.51) and crude protein content (9.51); cluster VI for leaf: stem ratio (0.37) and green fodder yield per plant (292.63); cluster II for number leaves per plant (55.45); cluster III for number of tillers per plant (10.21) and cluster VIII for leaf length (51.65).

4.4 CORRELATION COEFFICIENTS

Correlation coefficients at genotypic and phenotypic levels have been presented in Table 12. In general, the genotypic correlations were of higher in magnitude as compared to their corresponding phenotypic correlations in all the environments and also in pooled basis. A critical perusal of correlation coefficients revealed that the green fodder yield was found positively and significantly associated with plant height, stem diameter, leaves per plant, leaf length, leaf breadth, and dry fodder yield per plant and negatively correlated with leaf: stem ratio in E_2, E_3 and E_4 environments as well as on pooled basis. Non-significant association was observed for green fodder yield with days to 50 per cent flowering and crude protein content in all the environments and with IVDMD in E_1 and E_4, whereas IVDMD was positively and significantly correlated with green fodder yield in E_2 and E_3.

Days to 50 per cent flowering exhibited positive association with stem diameter, leaf breadth, leaf: stem ratio in E_4 and pooled analysis. whereas, it had positive and significant association with number of leaves per plant in E_1, leaf: stem ratio in E_3, E_4 and pooled basis. crude protein content in E_1 and E_3 and IVDMD in E_3. However, days to 50 per cent flowering was negatively correlated with crude protein content in E_2.

Table 12: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients amongst green fodder yield, its components and quality characters in oats

Character		Days to 50% flowering	Plant height (cm)	No. of tillers/ plant	Stem diameter (mm)	No. of leaves/ plant	Leaf length (cm)	Leaf breadth (cm)	Leaf: stem ratio	Dry fodder yield/ plant (g)	Crude protein content (%)	*In vitro* dry matter digestibility (%)	Green fodder yield/ plant (g)
Days to 50% flowering	E_1	-	0.0185	0.0444	0.1346	0.3481	-0.0261	0.2023	0.1889	-0.0021	0.3357	0.2675	0.1234
	E_2	-	0.2145	-0.1952	0.2346	-0.0547	0.1949	0.2050	0.0591	0.1024	-0.2792	-0.0233	0.1089
	E_3	-	0.2662	-0.0425	-0.0031	0.0999	0.2185	0.0579	0.3371	0.0443	0.2960	-0.4999	0.0372
	E_4	-	-0.1126	-0.0768	0.2831	0.0865	0.0250	0.2982	0.4533	-0.0926	0.1674	0.1669	0.0146
	P	-	0.2262	-0.0640	0.3394	0.2860	0.1523	0.3004	0.4226	0.1544	0.1722	0.2945	0.2337
Plant height (cm)	E_1	0.0175	-	-0.4293	0.6175	-0.1063	0.5158	0.6838	-0.2812	0.5544	-0.0135	0.0542	0.4816**
	E_2	0.2113	-	-0.3652	0.5076	-0.0202	0.4597	0.3947	-0.2727	0.7119	-0.1818	-0.0581	0.6879**
	E_3	0.2587	-	-0.3232	0.4377	-0.1355	0.2759	0.5533	-0.4523	0.7215	-0.0832	-0.0672	0.5481**
	E_4	-0.1050	-	-0.4116	0.3274	-0.2922	0.6828	0.5774	-0.3928	0.5756	-0.1533	0.0852	0.5345**
	P	0.2346	-	-0.4265	0.6039	-0.1884	0.5708	0.6835	-0.3689	0.7588	-0.1298	-0.0113	0.6826**
No. of tillers/plant	E_1	0.0355	-0.4149**	-	-0.2744	0.7703	-0.0247	-0.4928	0.2116	0.0807	-0.2491	0.0098	0.1648
	E_2	-0.1888	-0.3408*	-	-0.2240	0.8160	-0.2857	-0.3071	0.1504	0.1427	0.0798	0.2575	0.1842
	E_3	-0.0375	-0.3000*	-	-0.2858	0.8678	-0.0809	-0.1897	0.3352	0.0680	0.0555	0.2437	0.2315
	E_4	-0.0758	-0.4013**	-	-0.2855	0.9070	-0.5082	-0.3437	0.1342	0.1939	0.1609	-0.0768	0.2539
	P	-0.0632	-0.4173**	-	-0.4394	0.8343	-0.3186	-0.4682	0.2587	-0.1217	0.0111	0.1227	-0.0092
Stem diameter (mm)	E_1	0.1224	0.5680**	-0.2430	-	0.1318	0.5576	0.7998	0.1362	0.6004	0.0805	0.2998	0.6165**
	E_2	0.2229	0.4705**	-0.2078	-	0.1092	0.2249	0.8277	0.0400	0.5928	0.1887	0.3373	0.5886**
	E_3	0.0013	0.4056**	-0.2739*	-	-0.0492	0.0527	0.8619	-0.1435	0.4870	0.1175	0.1780	0.5367**
	E_4	0.2799*	0.3056*	-0.2702*	-	-0.0352	0.3201	0.8184	0.1975	0.3853	0.3788	0.3089	0.4161**
	P	0.3294*	0.5844**	-0.4159**	-	-0.0095	0.3582	0.9012	0.0768	0.6311	0.2615	0.3565	0.6701**
No. of leaves/plant	E_1	0.3302*	-0.1180	0.7699**	0.1064	-	0.1033	-0.0761	0.4024	0.2826	-0.0153	0.3061	0.4066**
	E_2	-0.0553	-0.0303	0.7935**	0.0987	-	-0.1541	0.0107	0.3925	0.2930	0.2654	0.4064	0.3669**
	E_3	0.0943	-0.1206	0.8522**	-0.0533	-	0.0165	0.0517	0.3781	0.2832	0.1427	0.3725	0.4902**
	E_4	0.0802	-0.2891*	0.8970**	-0.0348	-	-0.3126	-0.1105	0.3088	0.3506	0.2608	-0.0349	0.4173**
	P	0.2802*	-0.1877	0.8245**	-0.0094	-	-0.1369	-0.0922	0.4738	0.3258	0.1851	0.3021	0.2987*
Leaf length(cm)	E_1	-0.0270	0.4982**	-0.0176	0.5196**	0.1009	-	0.3921	0.3226	0.4754	-0.2559	-0.0142	0.4882**
	E_2	0.1883	0.4504**	-0.2788*	0.2072	-0.1516	-	0.3034	-0.0812	0.3023	-0.2791	-0.0053	0.2970*
	E_3	0.2149	0.2777*	-0.0763	0.0648	0.0061	-	0.1451	0.1319	0.3223	-0.3203	-0.0446	0.3314*
	E_4	0.0339	0.6533**	-0.4753**	0.2829*	-0.2915*	-	0.4904	-0.0171	0.2802	-0.1680	0.2402	0.3082*
	P	0.1508	0.5520**	-0.2957*	0.3500*	-0.1299	-	0.3698	0.0508	0.4553	-0.3259	0.0075	0.4123**

Continue.....

Character		Days to 50% flowering	Plant height (cm)	No. of tillers/ plant	Stem diameter (mm)	No. of leaves/ plant	Leaf length (cm)	Leaf breadth (cm)	Leaf: stem ratio	Dry fodder yield/ plant (g)	Crude protein content (%)	*In vitro* dry matter digestibility (%)	Green fodder yield/ plant (g)
Leaf breadth (cm)	E_1	0.1926	0.6452**	-0.4334**	0.7273**	-0.0716	0.3714**	-	0.1073	0.4287	0.1604	0.1547	0.4545**
	E_2	0.1865	0.3718**	-0.2723*	0.7186**	0.0051	0.2858*	-	0.0604	0.4790	0.2635	0.3451	0.5078**
	E_3	0.0483	0.5137**	-0.1506	0.7590**	0.0514	0.1311	-	-0.0273	0.6097	0.1386	0.2121	0.6460**
	E_4	0.2795*	0.5368**	-0.3173*	0.7216**	-0.1092	0.4380**	-	-0.0179	0.5361	0.2584	0.3066	0.4923**
	P	0.2787*	0.6478**	-0.4259**	0.8422**	-0.0889	0.3472*	-	-0.0208	0.5995	0.2087	0.2381	0.6275**
Leaf: stem ratio	E_1	0.1607	-0.2690	0.2197	0.1059	0.3870**	0.2912*	0.0987	-	0.0052	-0.0488	0.1640	0.1088
	E_2	0.0612	-0.2510	0.1306	0.0037	0.3506*	-0.0688	0.0533	-	-0.1947	0.3089	0.1119	-0.1241
	E_3	0.3087*	-0.4097**	0.2828*	-0.1138	0.3251*	0.1153	-0.0151	-	-0.3795	0.1727	0.3410	-0.2107
	E_4	0.4379**	-0.3846**	0.1284	0.1789	0.2996*	-0.0138	-0.0071	-	-0.2663	0.2735	0.3452	-0.1437
	P	0.4045**	-0.3578**	0.2459	0.0632	0.4578**	0.0381	-0.0153	-	-0.2114	0.2268	0.3101	-0.0647
Dry fodder yield/ plant (g)	E_1	-0.0051	0.5306**	0.1271	0.5442**	0.2853*	0.4566**	0.3988**	0.0262	-	-0.1801	0.0044	0.9234**
	E_2	0.0955	0.6851**	0.1650	0.5340**	0.3112*	0.2947*	0.4531**	-0.1722	-	0.0815	0.2427	0.9588**
	E_3	0.0415	0.7052**	0.1108	0.4474**	0.3128*	0.3005*	0.5591**	-0.3531**	-	-0.0970	0.0927	0.8930**
	E_4	-0.0905	0.5515**	0.2232	0.3537**	0.3659**	0.2782*	0.4818**	-0.2533	-	0.2087	0.0800	0.9475**
	P	0.1500	0.7436**	-0.0948	0.6065**	0.3183*	0.4401**	0.5679**	-0.2054	-	-0.0476	0.0866	0.9357**
Crude protein content (%)	E_1	0.2961*	-0.0167	-0.2054	0.0400	-0.0063	-0.2401	0.1351	-0.0440	-0.1623	-	0.5273	-0.1035
	E_2	-0.2733*	-0.1729	0.0747	0.1621	0.2455	-0.2561	0.2395	0.2991*	0.0766	-	0.4075	0.1105
	E_3	0.2712*	-0.0798	0.0554	0.1047	0.1394	-0.2982*	0.1479	0.1634	-0.0803	-	0.6346	0.0579
	E_4	0.1317	-0.1432	0.1245	0.3533**	0.2285	-0.1671	0.2285	0.2881*	0.1696	-	0.3988	0.2387
	P	0.1600	-0.1266	0.0033	0.2551	0.1707	-0.3116*	0.1966	0.2173	-0.0480	-	0.5998	0.0659
In vitro dry matter digestibility (%)	E_1	0.2293	0.0482	0.0164	0.2300	0.2739*	-0.0277	0.1310	0.1373	0.0081	0.4993**	-	0.1622
	E_2	-0.0330	-0.0530	0.2213	0.2558	0.3373*	0.0051	0.2831*	0.1465	0.2092	0.4534**	-	0.2934*
	E_3	0.4435**	-0.0541	0.2061	0.1509	0.3410*	-0.0466	0.1909	0.2784*	0.0888	0.6590**	-	0.3061*
	E_4	0.1134	0.0692	-0.0877	0.2760*	-0.0402	0.1818	0.2819*	0.2933*	0.0421	0.4987**	-	0.1482
	P	0.2728*	-0.0114	0.0935	0.3385*	0.2745*	0.0027	0.2207	0.2958*	0.0783	0.6078**	-	0.2406
Green fodder yield/plant (g)	E_1	0.1155	0.4568**	0.2085	0.5556**	0.4250**	0.4671**	0.4219**	0.1214	0.9254**	-0.0913	0.1396	-
	E_2	0.1023	0.6650**	0.2000	0.5358**	0.3811**	0.2840*	0.4820**	-0.1086	0.9583**	0.1052	0.2827*	-
	E_3	0.0343	0.5375**	0.2645	0.4918**	0.5114**	0.3045*	0.5935**	0.2002	0.8961**	0.0600	0.2750*	-
	E_4	0.0116	0.5178**	0.2752*	0.3840**	0.4298**	0.2916*	0.4482**	-0.1369	0.9452**	0.2053	0.1094	-
	P	0.2290	0.6721**	0.0124	0.6459**	0.3090*	0.4026**	0.5930**	-0.0620	0.9351**	0.0595	0.2207	-

*, ** Significant at P=0.05 and P=0.01, respectively; P= Pooled analysis

Plant height had positive and significant association with stem diameter, leaf length, leaf breadth and dry fodder yield per plant in all the four environments and in pooled analysis. Plant height was negatively correlated with number of tillers per plant and leaf: stem ratio in all the environments and on the basis of pooled data.

Number of tillers per plant showed significant positive association with number of leaves per plant in all the environments, whereas, positive significant association was found with leaf: stem ratio in E_3 and with green fodder yield in E_4. However, negative significant association was observed with stem diameter in E_3, E_4 and pooled, leaf length in E_2, E_4 and pooled, leaf breadth in E_1, E_2, E_4 and pooled analysis.

Stem diameter showed significant and positive association with leaf breadth and dry fodder yield per plant in all the four environments as well as in pooled analysis. Leaf length had positive and significant association with stem diameter in E_1, E_4 and on pooled basis, whereas positive and significant association of stem diameter was observed in E_4 with crude protein content and IVDMD.

Number of leaves per plant were positively and significantly correlated with leaf: stem ratio, dry fodder yield per plant and IVDMD in all the environments except E_4 in case of IVDMD. On the basis of pooled analysis, number of leaves per plant was significantly correlated with leaf: stem ratio and IVDMD, whereas it was negatively correlated with leaf length in E_4.

Leaf length had positive and significant association with leaf breadth in E_1, E_2, E_4 and pooled basis, leaf: stem ratio in E_1, whereas it had significant and positive association with dry fodder yield per plant in all the environments and in pooled basis. However, leaf length was negatively correlated with crude protein content in E_3 and pooled analysis.

Positive and significant association of leaf breadth was observed with dry fodder yield per plant in all the four environments as well as on the basis of pooled analysis. However, leaf breadth showed a significant positive association with IVDMD in E_2 and E_4 only.

Leaf: stem ratio showed significant and positive association with crude protein content in E_2 and E_4, and IVDMD in E_3, E_4 and pooled analysis. However, it had negative and significant association with dry fodder yield in E_3.

Dry fodder yield per plant was observed to be significantly and positively correlated with green fodder yield per plant in all the environments as well as in pooled basis.

Crude protein content showed a positive and significant association with IVDMD in all the four environments.

4.5 PATH-COEFFICIENT ANALYSIS

Path-coefficient analysis provides more realistic and clear picture of the contribution of independent variables in the manifestation of dependent one that remains hardly detectable at correlation level. Since, it takes into consideration the direct as well as indirect effect of one variable through the other on the dependent characters. Only those characters were taken into consideration for estimation of path-coefficients, which had significant correlation with green and dry fodder yield and their estimates are given in Table 13.

Plant height had positive and high direct effect in all the environments. However, it contributed indirectly via stem diameter in E_1, E_4 and pooled basis, via leaf breadth in E_2 and E_3.

The direct contribution of stem diameter was positive and high in all the environments except E_3. However, indirect effect was high via leaf breadth in E_3, but major contribution was recorded via plant height in all the environments as well as on pooled basis.

Table 13: Direct and Indirect effects of various characters on green and dry fodder yield in oats

Character		Days to 50% flowering	Plant height (cm)	No. of tillers/ plant	Stem diameter (mm)	No. of leaves/ plant	Leaf length (cm)	Leaf breadth (cm)	Leaf: stem ratio	'r' with GFY
Days to 50% flowering	E_1	-0.0066	0.0046	0.0151	0.0529	0.0526	-0.0370	0.0229	-0.0150	0.1234
	E_2	-0.0270	0.1184	-0.0312	0.0262	-0.0149	-0.0113	0.0562	-0.0076	0.1089
	E_3	0.0020	0.0250	0.0071	0.0001	-0.0776	0.0378	0.0284	-0.1406	0.0372
	E_4	0.0341	-0.0700	-0.0106	0.0802	0.0540	-0.0321	-0.0324	-0.0757	0.0146
	P	-0.0932	0.1086	-0.0388	0.1810	0.1023	0.0143	-0.0277	-0.0427	0.2337
Plant height (cm)	E_1	-0.0301	**0.2504**	-0.1457	0.2426	-0.0161	0.0588	0.0773	0.0144	0.4816**
	E_2	-0.0267	**0.5521**	-0.0264	0.0566	-0.0055	-0.0270	0.1084	0.0351	0.6879**
	E_3	0.0005	**0.0934**	0.0541	-0.0025	-0.1053	0.0477	0.2715	0.1886	0.5481**
	E_4	-0.0095	**0.6220**	-0.0031	0.0961	-0.1836	-0.0552	-0.0047	0.0656	0.5345**
	P	-0.0211	**0.4804**	-0.0589	0.3221	-0.0674	0.0534	-0.0631	0.0373	0.6826**
No. of tillers/ plant	E_1	-0.0003	-0.1075	**0.3394**	-0.1078	0.1165	-0.0028	-0.0557	-0.0169	0.1648
	E_2	0.0053	-0.0911	**0.1597**	-0.0249	0.2226	0.0166	-0.0843	-0.0194	0.1842
	E_3	-0.0001	-0.0302	**-0.1674**	0.0017	0.6744	-0.0140	-0.0930	-0.1398	0.2315
	E_4	-0.0023	-0.2560	**0.0075**	-0.0838	0.5670	0.0411	0.0028	-0.0224	0.2539
	P	0.0099	-0.2048	**0.1383**	-0.2343	0.2984	-0.0298	0.0432	-0.0261	-0.0092
Stem diameter (mm)	E_1	-0.0009	0.1546	-0.0931	**0.3928**	0.0199	0.0535	0.0904	-0.0108	0.6165**
	E_2	-0.0063	0.2803	-0.0857	**0.1116**	0.0298	-0.0131	0.2273	-0.0051	0.5886**
	E_3	-0.0001	0.0409	0.0479	**-0.0058**	-0.0382	0.0091	0.4230	0.0599	0.5367**
	E_4	0.0085	0.2036	-0.0022	**0.2936**	-0.0219	-0.0259	-0.0066	-0.0330	0.4161**
	P	-0.0316	0.2901	-0.0608	**0.5332**	-0.0034	0.0335	-0.0832	-0.0078	0.6701**
No. of leaves/ plant	E_1	-0.0023	-0.0266	0.2614	0.0518	**0.1512**	0.0118	-0.0086	-0.0321	0.4066**
	E_2	0.0015	-0.0112	0.1303	0.0122	**0.2728**	0.0089	0.0029	-0.0505	0.3669**
	E_3	0.0002	-0.0127	-0.1453	0.0003	**0.7771**	0.0029	0.0254	-0.1577	0.4902**
	E_4	0.0027	-0.1817	0.0068	-0.0103	**0.6252**	0.0253	0.0009	-0.0516	0.4173**
	P	-0.0266	-0.0905	0.1154	-0.0051	**0.3577**	-0.0128	0.0085	-0.0478	0.2987*
Leaf length (cm)	E_1	0.0002	0.1292	-0.0084	0.2191	0.0156	**0.1139**	0.0443	-0.0257	0.4882**
	E_2	-0.0053	0.3120	-0.0454	0.0251	-0.0420	**-0.0412**	0.0833	0.0105	0.2970*
	E_3	0.0004	0.0858	0.0135	-0.0003	0.0128	**0.2029**	0.0712	-0.0550	0.3314*
	E_4	0.0008	0.4247	-0.0038	0.0940	-0.1266	**-0.0808**	-0.0039	0.0038	0.3082*
	P	-0.0142	0.2742	-0.0441	0.1910	-0.0490	**0.0935**	-0.0341	-0.0051	0.4123**
Leaf breadth (cm)	E_1	-0.0013	0.1712	-0.1672	0.3142	-0.0115	0.0447	**0.1131**	-0.0085	0.4545**
	E_2	-0.0055	0.2179	-0.0490	0.0923	0.0029	-0.0176	**0.2746**	-0.0078	0.5078**
	E_3	0.0001	0.0517	0.0318	-0.0050	0.0401	0.0251	**0.4908**	0.0114	0.6460**
	E_4	0.0093	0.3592	-0.0026	0.2403	-0.0691	-0.0396	**-0.0081**	0.0030	0.4923**
	P	-0.0280	0.3284	-0.0648	0.4806	-0.0329	0.0346	**-0.0923**	0.0021	0.6275**
Leaf: stem ratio	E_1	-0.0013	-0.0453	0.0718	0.0535	0.0608	0.0367	0.0121	**-0.0796**	0.1088
	E_2	-0.0016	-0.1506	0.0240	0.0045	0.1071	0.0047	0.0166	**-0.1287**	-0.1241
	E_3	0.0007	-0.0423	-0.0561	0.0008	0.2939	0.0228	-0.0134	**-0.4170**	-0.2107
	E_4	0.0141	-0.2443	0.0010	0.0580	0.1930	0.0014	0.0001	**-0.1669**	-0.1437
	P	-0.0394	-0.1772	0.0358	0.0410	0.1695	0.0048	0.0019	**-0.1010**	-0.0647

GFY = Green Fodder Yield: 'r'= Genotypic correlation coefficient; P=Pooled analysis;
Residual effect E_1:0.4222; E_2:0.2854; E_3:0.1630; E_4: 0.2813; P: 0.2437

Character		Days to 50% flowering	Plant height (cm)	No. of tillers/ plant	Stem diameter (mm)	No. of leaves/ plant	Leaf length (cm)	Leaf breadth (cm)	Leaf: stem ratio	'r' with DFY
Days to 50% flowering	E_1	-0.0472	0.0089	0.0214	0.0701	-0.0370	0.0001	-0.0142	-0.0039	-0.0021
	E_2	-0.0333	0.1230	-0.0390	0.0511	-0.0088	-0.0170	0.0359	-0.0092	0.1024
	E_3	-0.0255	0.0885	0.0016	0.0002	0.0494	0.0491	0.0241	-0.1430	0.0443
	E_4	-0.1220	-0.0559	0.0218	0.0120	0.0717	-0.0035	0.0918	-0.1086	-0.0926
	P	-0.0924	0.1356	-0.0159	0.1982	0.0829	0.0155	-0.0664	-0.0527	0.1544
Plant height (cm)	E_1	-0.0006	**0.4760**	-0.2067	0.3215	0.0113	-0.0023	-0.0481	0.0037	0.5544**
	E_2	-0.0071	**0.5733**	-0.0330	0.1105	-0.0032	-0.0402	0.0691	0.0426	0.7119**
	E_3	-0.0068	**0.3324**	0.0122	-0.0336	-0.0670	0.0620	0.2305	0.1919	0.7215**
	E_4	0.0137	**0.4965**	0.1171	0.0145	-0.2425	-0.0957	0.1778	0.0942	0.5756**
	P	-0.0209	**0.5994**	-0.1065	0.3526	-0.0216	0.0580	-0.1512	0.0461	0.7588**
No. of tillers/ plant	E_1	-0.0021	-0.2043	**0.4816**	-0.1428	-0.0620	0.0001	0.0347	-0.0043	0.0807
	E_2	0.0065	-0.0947	**0.1998**	-0.0487	0.1322	0.0250	-0.0537	-0.0235	0.1427
	E_3	0.0011	-0.1074	**-0.0378**	0.0220	0.4296	-0.0182	-0.0790	-0.1422	0.0680
	E_4	0.0094	-0.2043	**-0.2845**	-0.0126	0.7528	0.0712	-0.1058	-0.0821	0.1939
	P	0.0059	-0.2556	**0.2497**	-0.2565	0.0960	-0.0323	0.1036	-0.0323	-0.1217
Stem diameter (mm)	E_1	-0.0063	0.2939	-0.1321	**0.5206**	-0.0140	-0.0025	-0.0563	-0.0028	0.6004**
	E_2	-0.0078	0.2911	-0.0447	**0.2177**	0.0177	-0.0197	0.1448	-0.0062	0.5928**
	E_3	0.0001	0.1455	0.0108	**-0.0768**	-0.0243	0.0118	0.3590	0.0609	0.4870**
	E_4	-0.0333	0.1626	0.0812	**0.0442**	-0.0292	-0.0448	0.2521	-0.0473	0.3853**
	P	-0.0313	0.3620	-0.1097	**0.5839**	-0.0010	0.0364	-0.1993	-0.0095	0.6311**
No. of leaves/ plant	E_1	-0.0164	-0.0506	0.3709	0.0686	-0.1065	-0.0005	0.0054	-0.0082	0.2826*
	E_2	0.0018	-0.0115	0.1630	0.0238	**0.1620**	0.0135	0.0019	-0.0513	0.2930*
	E_3	-0.0025	-0.0450	-0.0328	0.0038	**0.4950**	0.0037	0.0215	-0.1604	0.2832*
	E_4	-0.0105	-0.1451	-0.2580	-0.0015	**0.8300**	0.0438	-0.0340	-0.0740	0.3505*
	P	-0.0264	-0.1129	0.2083	-0.0055	**0.3150**	-0.0139	0.0204	-0.0591	0.3258*
Leaf length (cm)	E_1	0.0012	0.2455	-0.0119	0.2903	-0.0110	**-0.0045**	-0.0276	-0.0066	0.4754**
	E_2	-0.0065	0.3635	-0.0570	0.0490	-0.0250	**-0.0875**	0.0531	0.0127	0.3023*
	E_3	-0.0056	0.0917	0.0031	-0.0040	0.0082	**0.2245**	0.0604	-0.0559	0.3223*
	E_4	-0.0030	0.3400	0.1500	0.0271	-0.2490	**-0.1400**	0.1510	0.0041	0.2802*
	P	-0.0140	0.3421	-0.0795	0.2091	-0.0157	**0.1016**	-0.0818	-0.0063	0.4553**
Leaf breadth (cm)	E_1	-0.0095	0.3254	-0.2373	0.4165	0.0081	-0.0018	**-0.0705**	-0.0022	0.4287**
	E_2	-0.0068	0.2263	-0.0514	0.1802	0.0017	-0.0265	**0.1750**	-0.0094	0.4790**
	E_3	-0.0015	0.1839	0.0072	-0.0662	0.0256	0.0326	**0.4166**	0.0116	0.6097**
	E_4	-0.0364	0.2867	0.0978	-0.0361	-0.0916	-0.0587	**0.3080**	0.0043	0.5361**
	P	-0.0277	0.4097	-0.1169	0.5262	-0.0106	0.0376	**-0.2212**	0.0026	0.5995**
Leaf: stem ratio	E_1	-0.0089	-0.0862	0.1019	0.0709	-0.0428	-0.0014	-0.0076	**-0.0206**	0.0052
	E_2	-0.0020	-0.1564	0.0300	0.0087	0.0636	0.0071	0.0106	**-0.1564**	-0.1947
	E_3	-0.0086	-0.1503	-0.0127	0.0110	0.1872	0.0296	-0.0114	**-0.4243**	-0.3795
	E_4	-0.0553	-0.1950	-0.0381	0.0087	0.2563	0.0024	-0.0055	**-0.2397**	-0.2663
	P	-0.0390	-0.2211	0.0545	0.0448	0.0545	0.0052	0.0046	**-0.1249**	-0.2114

DFY = Dry Fodder Yield: 'r'= Genotypic correlation coefficient; P=Pooled analysis;
Residual effect E_1:0.4449; E_2:0.2936; E_3:0.1737; E_4: 0.2562; P: 0.2686

The number of leaves per plant had positive and high direct effect on green fodder yield in all the environments as well as in pooled analysis, whereas it contributed indirectly via number of tillers per plant in E_1, E_2 and pooled analysis, via leaf length in E_4 and leaf breadth in E_3.

Leaf length exhibited positive direct effect in E_1, E_3 and pooled, although it had negative in E_2 and E_4. However, major contribution was recorded via plant height in all the environments. Indirect effect was high via stem diameter in E_1 only.

Contribution of leaf breadth was positive and high in E_1, E_2 and E_3, whereas it was negative in E_4 and pooled analysis. However, indirect effect was recorded maximum via plant height in E_2, E_3 and E_4, via stem diameter in E_1 and pooled analysis.

Plant height had positive and high direct effects with dry fodder yield in all the environments as well as in pooled analysis. However, indirect effect was high via stem diameter in E_1, E_2 and pooled, via leaf breadth in E_3 and E_4.

Direct effect of stem diameter was positive and high in E_1, E_2, E_4 and pooled, whereas it was negative in E_3, but major contribution (positive indirect effect) was recorded via plant height. However, positive and high indirect effect was recorded via leaf breadth in E_3 and E_4.

Number of leaves per plant showed positive and high direct effects in all the environments except E_1. However, it contributed via number of tillers per plant in E_1, E_2 and pooled basis and via stem diameter in E_3 and leaf length in E_4.

Although leaf length exhibited negative direct effects in E_1, E_2 and E_4, whereas it was positive in E_3 and pooled. However indirect effect was positive and high via plant height in all the environments.

Leaf breadth had positive and high direct effect in E_2, E_3 and E_4, whereas it had negative direct effects in E_1 and pooled analysis,

but indirectly contributed via plant height in all the 4 environments as well as in pooled basis.

4.6 STABILITY ANALYSIS

4.6.1 Joint regression analysis:

The mean squares due to genotypes were highly significant against pooled error as well as remainder for all the characters. This indicated that sufficient genetic variability for various traits was present among the genotypes. Environmental mean squares were also highly significant against pooled error and remainder indicating differences among the environments, which revealed that environments chosen in this study were highly variable. Significance of G x E interaction mean squares for all the characters against pooled error indicated presence of G x E interaction (Table 14). Further, partitioning of G x E interactions, into heterogeneity between regression and remainder showed that mean squares due to these components were significant for all the characters against pooled error mean square.

Mean square due to heterogeneity between regression tested against remainder mean square were significant for days to 50 per cent flowering, plant height, tillers per plant, number of leaves per plant, green and dry fodder yield per plant and IVDMD. This indicated preponderance of linear component in these characters and hence, prediction appeared possible. Nevertheless, these characters had both linear and non-linear component of G x E interactions. However, non-linear component was higher than linear component for stem diameter, leaf length, leaf breadth, leaf: stem ratio and crude protein content indicating that prediction could not be made easily for these characters. However, it could be done by considering individual genotype.

The environmental indices for each character over four environments expressed as deviation from general mean are presented

Table 14: Joint regression analysis for fodder yield, its components and quality characters in oats according to 1. Perkins and Jinks (1968a) and 2. Eberhart and Russell (1966)

	Sources	D.F.	Mean sum of squares											
			Days to 50% flowering	Plant height (cm)	No. of tillers/ plant	Stem diameter (mm)	No. of leaves/ plant	Leaf length (cm)	Leaf breadth (cm)	Leaf: stem ratio	Green fodder yield/ plant (g)	Dry fodder yield/ plant (g)	Crude protein content (%)	IVDMD (%)
1.	Genotypes	49	48.682**+-	516.128**+-	9.069**++	2.572**+-	302.224**++	84.703**++	0.276**++	0.0100**++	9651.866**++	443.149**++	2.034**++	40.279**++
	Environment Joint regression	3	11939.667**+-	2976.193**+-	199.986**++	11.661**++	5449.098**++	220.547**++	0.862**++	0.0293**++	752798.857**++	28671.395**++	3.916**++	188.280**++
	G x E	147	17.266**+	42.405**+-	1.106**++	0.355**	40.335**++	9.151**	0.018**	0.0014**	2002.720**++	94.419**++	0.108**	3.446*++
	Heterogeneity between regression	49	18.106**+	50.405**++	1.623**++	0.298**	60.253**++	6.943**	0.013**	0.0010**	4333.638**++	212.617**++	0.080**	3.497**++
	Remainder	98	16.846**	38.405**	0.847**	0.383**	30.376**	10.256**	0.021**	0.0017**	837.261**	35.320**	0.123**	1.920
	Pooled error	392	0.917	3.427	0.327	0.125	5.277	1.380	0.009	0.0004	143.522	6.579	0.079	3.375
2.	Genotypes	49	48.682**++	516.128**++	9.069**++	2.572**++	302.224**++	84.703**++	0.276**++	0.0100**++	9651.866**++	443.149**++	2.034**++	40.279**++
	Environment + (G x E)	150	255.714**++	101.081**++	5.083**++	0.581**++	148.510**++	13.379**++	0.035**++	0.0020**+	17018.643**++	665.959**++	0.185**++	6.162**++
	Environment (linear)	1	35819.00**++	8928.58**++	599.95**++	34.98**++	16347.29**++	661.64**++	2.58**++	0.088**++	2258396.57**++	86014.18**++	11.74**++	564.84**++
	G x E (linear)	49	18.106**+	50.405**++	1.623**++	0.298**	60.253**++	6.943**	0.013**	0.0010**	4333.638**++	212.617**++	0.080**	3.497**++
	Pooled deviation	100	16.509**	37.637**	0.830**	0.375**	29.769**	10.050**	0.020**	0.0020**	820.516**	34.614**	0.120**	1.882
	Pooled error	392	0.917	3.427	0.327	0.125	5.277	1.380	0.009	0.0004	143.522	6.579	0.079	3.375

*, **Significant against pooled error at P=0.05 and P=0.01; +, ++ Significant against remainder at P=0.05 and P=0.01, respectively; G x E = Genotype x Environment

in Table 15. The data revealed that E_1 was the best for all the characters, whereas E_2 was good for number of tillers and leaves per plant and leaf: stem ratio. However, E_3 was best for days to 50 per flowering, plant height, stem diameter, leaf length, leaf breadth, crude protein content and IVDMD. In general, E_4 was the poor for most of the characters except days to 50 per cent flowering and leaf: stem ratio.

Table 15: Estimates of environmental index for each character in four environments expressed as deviation from grand mean (μ)

	Characters	E_1	E_2	E_3	E_4	μ
1.	Days to 50% flowering	3.80	-21.10	15.96	1.34	106.62
2.	Plant height (cm)	5.63	-6.25	7.65	-7.03	107.41
3.	No. of tillers/ plant	2.69	0.31	-1.73	-1.27	9.57
4.	Stem diameter (mm)	0.40	-0.14	0.36	-0.63	7.95
5.	No. of leaves/ plant	14.17	1.39	-9.01	-6.57	52.20
6.	Leaf length (cm)	2.66	-0.44	0.21	-2.44	48.39
7.	Leaf breadth (cm)	0.12	-0.04	0.08	-0.17	2.27
8.	Leaf: stem ratio	0.02	0.02	-0.03	0.00	0.33
9.	Green fodder yield/plant (g)	173.77	-58.08	-8.29	-107.39	266.69
10.	Dry fodder yield/plant (g)	33.85	-11.42	-1.41	-21.02	53.89
11.	Crude protein content (%)	0.26	-0.10	0.19	-0.36	8.87
12.	IVDMD (%)	1.80	-0.39	1.17	-2.56	64.75

4.6.2 Estimation of stability parameters of individual genotypes:

The estimates of stability parameters (mean, b_i and $S^{-2}d_i$) of 50 genotypes with respect to ten morphological and two quality characters are given in Tables 16 to 19 and described as follows:

Days to 50% flowering:

Five genotypes had non-significant b_i and $S^{-2}d_i$ values indicating absence of G x E interaction and 14 genotypes had significant b_i and $S^{-2}d_i$ values revealing the presence of linear and non-linear components of G x E interactions. Only three genotypes had linear component of G x E interaction, whereas 28 genotypes had non-linear component of G x E interactions, as $S^{-2}d_i$ alone was significant in case of these genotypes (Table 16).

Seven genotypes had b_i values >0, 10 genotypes were having <0 b_i values and 33 genotypes were having b_i values approaching to '0'

Table 16: Estimates of stability parameters for days to 50% flowering, plant height and number of tillers/plant in oats

Genotypes	Days to 50% flowering			Plant height (cm)			Number of tillers/plant		
	$\bar{X}$	bi	S^{-2} di	$\bar{X}$	bi	S^{-2} di	$\bar{X}$	bi	S^{-2} di
1. Kent	102.50	-0.15	64.89**	97.16	-0.09	67.24**	8.93	-0.39*	-0.06
2. DFO-54	99.91	0.12	5.91**	110.91	0.28	144.57**	9.77	-0.19	0.15
3. DFO-57	98.83	0.11	1.77*	99.50	-0.27	1.57	10.17	0.47*	-0.04
4. JHO-94-1	101.00	0.00	3.45**	88.91	0.17	34.75**	10.59	-0.63**	0.15
5. JHO-94-3	106.83	-0.03	12.11**	109.66	-0.32	28.63**	7.51	-0.22	-0.06
6. JHO-95-1	110.67	-0.03	3.92**	121.50	0.22	76.41**	8.60	-0.09	0.52*
7. JHO-95-2	110.41	0.13	7.96**	99.91	-0.39	10.81**	10.14	-0.61**	0.11
8. JHO-96-4	106.50	-0.22*	4.38**	114.00	0.40	-0.30	9.47	-0.20	-0.05
9. JHO-96-6	109.91	-0.05	6.25**	98.66	0.08	8.89**	11.15	0.23	0.11
10. JHO-97-4	109.75	0.24*	1.74*	93.16	-0.03	20.88**	11.75	0.10	1.74**
11. JHO-810	105.66	0.06	32.92**	86.00	-0.35	12.31**	10.73	-0.31*	1.45**
12. JHO-822	100.25	-0.07	21.01**	93.33	-0.47*	10.77**	11.44	0.23	0.28
13. JHO-829	100.75	0.21*	3.71**	95.41	0.13	65.30**	12.05	-0.49*	3.25**
14. JHO-851	108.08	0.13	12.97**	97.91	0.07	2.66	13.31	-0.27*	0.32
15. JHO-866	113.16	0.05	41.99**	99.83	-0.01	16.01**	10.11	0.01	-0.10
16. JHO-889	110.00	0.00	2.55**	124.75	-0.44	-0.67	10.44	0.35*	0.19
17. JHO-897	109.41	0.16*	0.41	99.75	-0.33	96.01**	10.20	0.09	1.60**
18. JHO-995	109.58	-0.03	1.01	109.25	0.47*	4.02	10.51	0.53*	1.41**
19. JHO-851E	110.16	0.11	7.05**	104.91	0.29	6.04*	11.97	-0.32*	1.99**
20. JHO-99-1	105.66	-0.19*	95.96**	112.00	0.19	13.13**	10.74	-0.67**	2.59**
21. JHO-99-2	103.08	-0.22*	37.55**	100.50	-0.65*	92.02**	10.02	-0.16	0.08
22. JHO-99-3	108.58	-0.22*	9.34**	119.25	0.18	18.24**	8.28	-0.05	0.72*
23. JHO-99-4	108.33	0.03	-0.24	108.41	0.05	4.13	6.95	0.09	0.10
24. JHO-99-5	106.83	-0.03	2.25**	102.66	0.52*	21.49**	9.31	0.17	0.03
25. JHO-99-6	108.50	0.13	42.95**	114.00	0.70*	66.26**	9.45	-0.46*	-0.03
26. JHO-99-7	108.00	0.23*	27.33**	98.08	-0.58*	26.89**	12.96	-0.11	3.44**
27. Blacknip	111.91	0.21*	38.71**	84.16	0.87*	34.01**	6.85	0.00	0.78**
28. S-2688	107.16	-0.15	60.48**	100.33	-0.38	42.68**	10.88	1.11**	-0.08
29. S-3021	109.83	0.00	44.90**	101.50	0.15	69.52**	10.11	1.05**	1.21**
30. UPO-212	106.33	0.11	41.89**	114.00	-0.68*	11.46**	9.69	-0.18	0.54*
31. UPO-230	105.91	0.25*	2.30**	115.83	-0.59*	26.04**	7.64	0.27*	0.93**
32. UPO-248	109.00	0.12	19.10**	114.25	1.17**	116.69**	7.65	-0.21	0.53*
33. UPO-250	101.08	0.13	50.78**	110.58	-0.10	30.26**	8.22	-0.09	0.68*
34. UPO-288	98.75	-0.21*	4.59**	103.08	-1.46**	5.79*	8.36	0.12	0.63*
35. OL-661	107.75	0.21*	8.79**	108.75	0.71*	-0.36	10.18	0.16	1.29**
36. OL-805	109.33	0.01	0.21	110.16	-0.09	20.48**	9.29	0.16	0.57*
37. OL-936	109.00	-0.06	1.46*	111.75	1.14**	143.74**	9.00	0.48*	0.70*
38. OS-6	105.66	-0.27*	0.97	103.25	-0.09	13.73**	8.80	0.43*	0.26
39. OS-7	107.16	-0.24*	-0.20	118.08	0.49*	76.63**	9.09	0.30*	0.09
40. OS-174	105.16	0.02	3.97**	111.50	-1.00**	98.69**	9.44	-0.15	0.60*
41. OS-189	106.50	0.15	18.21**	129.58	0.73*	4.41	8.50	-0.18	0.11
42. OS-237	108.50	0.03	3.07**	129.08	0.19	44.56**	8.65	-0.16	0.13
43. OS-242	111.00	-0.07	-0.18	125.50	0.54*	11.89**	8.27	0.05	0.51*
44. OS-245	106.75	-0.22*	22.04**	127.25	0.21	25.39**	7.05	0.00	0.37
45. OS-277	104.41	0.00	0.25	103.33	-0.34	4.76*	7.85	-0.36*	-0.02
46. OS-279	105.58	-0.11	6.60**	108.33	-0.42	27.44**	10.06	-0.11	1.43**
47. OS-285	103.83	-0.40**	13.96**	99.50	-0.44	31.05**	8.70	0.25	1.62**
48. OS-286	108.08	0.09	2.46**	110.33	0.11	2.36	7.54	0.17	1.25**
49. HJ-8	106.75	0.07	9.98**	133.41	0.22	0.18	9.20	-0.27*	0.94**
50. HFO-114	103.50	-0.18*	4.49**	97.41	-0.79*	17.05**	10.80	0.04	0.55*
Mean	106.62	0.00	-	107.41	0.00	-	9.57	0.00	-
S.E.	2.34	0.15	-	3.54	0.45	-	0.52	0.26	-

*, ** Significant at P=0.05 and 0.01, respectively

indicating their suitability to favourable, unfavourable and all types of environments, respectively. Eleven genotypes were early in flowering whereas 15 genotypes were late in flowering. However, 24 genotypes were medium in flowering. UPO-288 was earliest in flowering with below average response and was unstable. JHO-99-4 and OS-277 were medium in flowering whereas, JHO-995, OL-805 and OS-242 were found late in flowering with average response and found stable indicating their adaptability to all kind of environments. OS-6 and OS-7 were medium in flowering and showed their suitability for unfavourable environments. However, JHO-897 was late in flowering and suitable to favourable environments.

Plant height:

Both b_i and $S^{-2}d_i$ values were non-significant for plant height in 7 genotypes revealing the absence of G x E interaction. Three genotypes had significant b_i values indicating the presence of linear components of G x E interactions. On the other hand, 25 genotypes had non-linear component of G x E interactions as $S^{-2}d_i$ values were significant, whereas 15 genotypes had both b_i and $S^{-2}d_i$ values significant indicating the presence of linear and non-linear components of G x E interactions (Table 16).

Ten genotypes had b_i values >0 indicating their suitability to favourable environment, 8 genotypes were having <0 b_i values showed their adaptability for unfavourable/poor environments, whereas 32 genotypes were suitable to all kinds of environments as these were having b_i value approaching to '0'. Out of 50 genotypes, 17 genotypes had above average plant height, 23 genotypes below average plant height and 10 genotypes were average in plant height. HJ-8 had maximum plant height (133.41 cm) followed by OS-189 (129.58 cm), whereas Blacknip showed minimum plant height (84.16 cm). Out of 10 stable genotypes, above average plant height was exhibited by only 4 genotypes. Among them, HJ-8, JHO-889 and

JHO-96-4 had average response and OS-189 was having above average response indicating their adaptability for general and favourable environments, respectively. Genotypes OL-661 and JHO-995 were having average plant height showed their suitability for favourable environments, whereas JHO-99-4 and OS-286 suited for all type of environments. However, JHO-851 and DFO-57 had below average plant height and showed their adaptability to general environments.

Number of tillers/plant:

Simultaneous consideration of b_i and $S^{-2}d_i$ values revealed that 12 genotypes had non-significant values for these two parameters (Table 16). Nine genotypes had both b_i and $S^{-2}d_i$ significant revealing the presence of both linear and non-linear components of G x E interaction. Eleven genotypes had only linear component of G x E interactions, whereas 18 genotypes had only non-linear component.

Nine genotypes had b_i values greater than '0', 11 genotypes less than '0' indicating their adaptability for favourable and unfavourable/poor environments, respectively. Remaining 30 genotypes showed their suitability to all kind of environments as these genotypes were having their b_i values approaching to '0'. More than average tillering was observed in 20 genotypes, whereas 11 genotypes were average in tillering. However, below average tillering was recorded in 19 genotypes. JHO-851 had maximum number of tillers per plant (13.31; b_i = -0.27*) indicates their suitability to poor environments. Out of 23 stable genotypes with mean value above average, JHO-96-6, JHO-822 and JHO-866 showed their adaptability to a wide range of environments whereas, genotypes DFO-57, JHO-889 and S-2688 had high response indicating their capability to exploit in better environments. However, JHO-94-1, JHO-95-2 and JHO-851 having above average tillering and were well adapted to poor environments as their response was below in average ($b_i < 0$).

Stem diameter:

Based on the distribution of different genotypes on the basis of b_i and $S^{-2}d_i$, it is evident that regression coefficient was significant for six genotypes (Table 17) suggesting the presence of only linear component of G x E interaction. The significance of both the parameters in case of another six genotypes indicated that both linear and non-linear components accounted for the total G x E interaction. Twenty-three genotypes only had significant $S^{-2}d_i$ and hence, these genotypes had non-linear component of G x E interactions. Fifteen genotypes had non-significant regression coefficient and deviation from regression indicating the absence of G x E interaction.

Out of 50 genotypes, 21 were found stable as these were having non-significant $S^{-2}d_i$. Thirty-eight genotypes had average response, 4 genotypes above average and 8 genotypes were below average response indicating their adaptability to general, favourable and unfavourable environments, respectively. Above average stem diameter was recorded in 17 genotypes, whereas 16 genotypes were below average stem diameter. However, 17 genotypes showed average stem diameter. Maximum stem diameter was recorded in HJ-8 (9.74 mm) and OS-189 (9.48 mm) with average response (-0.50; 0.21, respectively). Eight genotypes having above average stem diameter and non-significant $S^{-2}d_i$, showed their suitability to all type of environments and these were JHO-99-6, JHO-99-7, Blacknip, UPO-230, UPO-250, OS-189, OS-245 and HJ-8. Genotypes OS-7 and OS-237 revealed their suitability to favourable environments. However, poor response was noticed in 3 genotypes namely JHO-889, JHO-897 and JHO-995.

Number of leaves/plant:

Stability parameters for number of leaves per plant (Table 17) indicated that eight genotypes had non-significant b_i and $S^{-2}d_i$ and showed absence of G x E interaction. Thirteen genotypes had

Table 17: Estimates of stability parameters for stem diameter, number of leaves/plant and leaf length in oats

Genotypes	Stem diameter (mm)			Number of leaves/plant			Leaf length (cm)		
	$\bar{X}$	bi	S^{-2} di	$\bar{X}$	bi	S^{-2} di	$\bar{X}$	bi	S^{-2} di
1. Kent	7.31	0.65	-0.01	42.91	-0.56*	2.94	49.75	-0.03	10.49**
2. DFO-54	8.40	0.15	0.94**	49.83	-0.23	4.29	52.25	0.33	3.24**
3. DFO-57	7.44	0.18	0.33**	51.91	0.34*	-0.02	53.75	0.07	10.95**
4. JHO-94-1	5.77	-0.80*	0.01	46.58	-0.67**	4.16	34.25	-0.54	1.08
5. JHO-94-3	8.00	-0.53	1.76**	40.58	-0.32*	-0.63	48.16	-1.24**	10.74**
6. JHO-95-1	8.22	-0.01	0.21*	47.50	-0.05	17.27**	49.50	-0.58	0.88
7. JHO-95-2	6.85	0.39	0.30**	54.08	-0.94**	19.47**	52.91	0.25	0.68
8. JHO-96-4	8.20	0.67	0.11	52.25	-0.14	1.95	48.33	0.04	1.27
9. JHO-96-6	8.04	-0.45	0.23*	66.33	0.88**	10.95*	48.50	0.28	10.56**
10. JHO-97-4	7.75	0.11	0.32**	69.08	0.14	66.96**	47.41	0.16	5.58**
11. JHO-810	6.93	0.66	0.37**	48.33	-0.27	21.60**	38.08	-1.20**	2.85*
12. JHO-822	7.41	-0.01	0.33**	55.58	-0.28	24.95**	49.33	-0.30	49.31**
13. JHO-829	6.42	-0.08	0.05	56.41	-0.77**	55.62**	34.50	-0.78	-0.25
14. JHO-851	6.56	0.42	0.55**	69.83	0.23	21.08**	44.75	0.68	10.29**
15. JHO-866	8.81	-1.23*	0.53**	60.41	-0.16	3.17	44.66	0.19	1.93*
16. JHO-889	8.84	-1.07*	0.13	66.16	0.62**	2.49	48.75	-0.30	0.57
17. JHO-897	8.61	-0.75*	-0.01	58.00	0.00	48.96**	45.66	0.64	12.10**
18. JHO-995	8.39	-0.89*	-0.04	52.33	0.39*	35.10**	46.08	0.33	9.95**
19. JHO-851E	7.31	0.29	0.05	64.33	-0.17	55.13**	48.00	1.02*	6.84**
20. JHO-99-1	8.03	-1.45*	1.79**	65.25	-0.46*	82.47**	42.25	-1.38**	2.04*
21. JHO-99-2	7.71	-0.03	0.10	50.33	-0.45*	3.85	43.50	-1.08*	3.99**
22. JHO-99-3	7.48	-1.00*	0.25*	46.58	-0.06	20.17**	49.00	-0.35	2.87*
23. JHO-99-4	8.20	-0.29	0.33**	37.50	0.03	5.07	46.25	-1.41**	5.00**
24. JHO-99-5	8.42	-0.77*	0.38**	56.83	0.59*	10.57*	46.41	0.85	15.29**
25. JHO-99-6	8.68	-0.35	0.03	53.58	-0.39*	2.40	50.58	-0.08	2.99*
26. JHO-99-7	8.38	-0.17	-0.03	78.75	0.20	179.96**	47.41	0.00	0.36
27. Blacknip	9.22	-0.13	0.06	48.66	0.93**	74.91**	42.25	0.55	1.02
28. S-2688	7.70	1.23*	0.34**	54.58	1.01**	-0.67	49.50	1.31*	44.27**
29. S-3021	7.66	0.21	1.00**	58.16	0.67**	53.30**	48.00	0.30	12.00**
30. UPO-212	7.80	-0.32	0.30**	53.00	-0.20	11.66*	54.92	0.97*	14.24**
31. UPO-230	8.79	0.01	0.09	42.00	0.37*	36.72**	43.91	-1.30**	1.40
32. UPO-248	8.24	-0.45	0.35**	42.83	0.06	31.36**	50.16	0.23	15.97**
33. UPO-250	8.60	0.33	0.01	47.75	0.00	26.56**	49.16	-0.10	14.91**
34. UPO-288	7.92	-0.31	0.28**	41.66	0.21	28.24**	45.00	-1.42**	43.09**
35. OL-661	7.13	-0.08	0.48**	53.25	0.05	54.51**	51.58	0.52	5.99**
36. OL-805	7.08	0.06	0.40**	51.66	-0.13	56.63**	50.33	0.82	19.00**
37. OL-936	7.95	0.38	0.23*	50.75	0.46*	33.60**	55.41	0.21	0.57
38. OS-6	7.13	0.63	0.44**	44.66	-0.15	1.08	48.50	-0.46	8.90**
39. OS-7	8.55	1.17*	0.09	50.91	0.18	0.95	49.50	-0.16	13.15**
40. OS-174	7.97	0.29	0.63**	49.00	-0.22	17.94**	50.41	-0.42	5.96**
41. OS-189	9.48	0.21	0.14	52.41	-0.46*	18.02**	53.25	-0.84	0.76
42. OS-237	9.05	0.76*	0.12	51.91	-0.19	3.97	52.58	-0.02	-0.38
43. OS-242	8.62	0.27	0.45**	47.83	0.38*	29.68**	52.50	0.06	15.15**
44. OS-245	8.92	0.37	0.02	39.41	0.05	12.54**	53.83	0.50	5.00**
45. OS-277	7.65	0.29	0.25*	36.83	-0.51*	-0.51	52.83	0.54	1.58
46. OS-279	6.94	2.05**	1.19**	50.00	-0.10	26.16**	49.33	0.79	33.86**
47. OS-285	7.52	0.16	0.07	48.41	-0.17	88.34**	48.83	0.79	10.32**
48. OS-286	7.87	0.20	0.57**	43.08	0.45*	27.40**	54.00	1.09*	11.71**
49. HJ-8	9.74	-0.50	-0.01	55.33	0.02	4.47	53.25	-0.40	3.37**
50. HFO-114	7.52	-0.48	0.00	54.50	-0.17	7.51*	50.33	0.84	4.86**
Mean	7.95	0.00	-	52.20	0.00	-	48.39	0.00	-
S.E.	0.35	0.73	-	3.15	0.30	-	1.83	0.87	-

*, ** Significant at P=0.05 and 0.01, respectively

significant b_i and $S^{-2}d_i$ indicating the presence of linear as well as non-linear components. Nine genotypes had significant b_i revealed the presence of linear portion of G x E interaction, whereas twenty genotypes had significant non-linear component ($S^{-2}d_i$).

Twelve genotypes had above average response, 10 genotypes below average response and 28 genotypes were average in response, which showed their suitability for favourable, unfavourable and general environments, respectively. Thirteen genotypes had above average mean performance, whereas, 19 genotypes had mean values below average. However, 18 genotypes were average in performance for this character. JHO-99-7 had maximum number of leaves per plant (78.75) especially suited to all type of environments due to its average response (b_i = 0.20) but this was unstable. Amongst seventeen stable genotypes, HJ-8 and JHO-866 were found ideal and showed adaptability to all types of environments, whereas JHO-889 exhibited high mean performance and above average responsiveness. Other stable genotypes with average mean were DFO-54, JHO-96-4, OS-7 and OS-237. Genotypes DFO-57 and S-2688 were well adapted to favourable environments, whereas JHO-99-2 and JHO-99-6 were adapted to unfavourable environments.

Leaf length:

A perusal of the b_i and $S^{-2}d_i$ values of 12 genotypes revealed absence of G x E interactions as both b_i and $S^{-2}d_i$ were non-significant in these genotypes. $S^{-2}d_i$ alone was significant in 27 genotypes indicating the presence of non-linear component. Ten genotypes had both linear and non-linear components of G x E interactions as b_i and $S^{-2}d_i$ of these genotypes were significant, whereas linear component of G x E interaction was observed in one genotype (Table 17).

Four genotypes had b_i values >0, another 7 genotypes were having <0 b_i values and remaining 39 genotypes had b_i values approaching to '0' indicating their suitability to favourable,

unfavourable and general environments, respectively. Seventeen genotypes had above average leaf length, and 14 genotypes below average leaf length. However, average leaf length was recorded in 19 genotypes. Maximum leaf length was recorded in OL-936 (55.41 cm). Out of 13 stable genotypes, above average leaf length was exhibited in case of 5 genotypes i.e. JHO-95-2, OL-936, OS-189, OS-237 and OS-277 indicating their adaptability to all type of environments, whereas JHO-95-1, JHO-96-4, JHO-889 and JHO-99-7 having average mean and stability. JHO-94-1, JHO-829 and Blacknip had below average leaf length but were found stable. However, UPO-230 was suitable for unfavourable environments.

Leaf breadth:

Simultaneous consideration of two stability parameters b_i and $S^{-2}d_i$ suggested the absence of G x E interactions in 27 genotypes as the estimates of both these parameters were non-significant in their cases. Linear component was present for 8 genotypes as shown by significant bi values (Table 18). In case of 2 genotypes, both b_i and $S^{-2}d_i$ were significant, whereas, 13 genotypes showed presence of non-linear component of stability.

Thirty five genotypes were found stable for leaf breadth as the estimates of $S^{-2}d_i$ were non-significant in these cases. Forty genotypes had average response ($b_i = 0$) indicating their adaptability to all types of environments. Five genotypes were having above average response ($bi>0$) which showed their suitability to favourable environments, whereas, another 5 genotypes were suitable for poor environments as these genotypes had below average response ($bi<0$). Out of 50 genotypes, 19 genotypes were below average leaf breadth, 15 genotypes had average leaf breadth and 16 genotypes had above average leaf breadth. Maximum leaf breadth was observed in HJ-8 (2.91 cm) followed by OS-189 (2.86 cm). Among stable genotypes, HJ-8 and JHO-99-7 exhibited high mean and below average

Table 18: Estimates of stability parameters for leaf breadth, leaf: stem ratio and green fodder yield/ plant in oats

Genotypes	Leaf breadth (cm)			Leaf: stem ratio			Green fodder yield/plant (g)		
	$\bar{X}$	bi	S^{-2} di	$\bar{X}$	bi	S^{-2} di	$\bar{X}$	bi	S^{-2} di
1. Kent	2.05	-0.27	0.00	0.36	0.62	0.001**	197.41	-0.27**	788.82**
2. DFO-54	2.41	-0.51	0.04**	0.29	-0.02	0.000	277.66	-0.22*	1447.23**
3. DFO-57	2.18	0.26	0.02*	0.37	0.20	0.002**	272.75	0.47**	134.52
4. JHO-94-1	1.78	0.36	0.00	0.27	-1.77*	0.002**	175.50	-0.74**	753.23**
5. JHO-94-3	2.35	-0.40	0.00	0.27	-0.45	0.000	236.75	-0.10	206.32*
6. JHO-95-1	2.49	-0.33	0.00	0.31	0.51	0.001**	283.17	-0.09	180.52
7. JHO-95-2	1.88	-0.05	0.02*	0.37	-0.81	0.000	218.66	-0.63**	548.30**
8. JHO-96-4	2.45	0.37	0.13**	0.28	-0.68	0.000	338.83	0.07	1016.57**
9. JHO-96-6	2.00	-0.08	0.01	0.40	0.76	0.001**	256.50	-0.01	215.65*
10. JHO-97-4	2.05	-0.48	0.01	0.41	-0.31	0.001**	254.16	0.10	1509.91**
11. JHO-810	1.99	0.25	0.01	0.32	0.96	0.000	176.16	-0.29**	514.20**
12. JHO-822	1.92	-0.56	0.04**	0.32	0.03	0.000	317.00	0.49**	68.39
13. JHO-829	1.89	-1.15**	0.00	0.28	-1.24*	0.000	203.50	-0.57**	393.06**
14. JHO-851	1.97	-0.11	0.04**	0.40	-0.29	0.002**	220.33	-0.25*	154.47
15. JHO-866	2.41	-0.06	0.00	0.36	-0.22	0.001**	266.58	-0.21*	2368.52**
16. JHO-889	2.50	0.01	0.00	0.30	0.95	0.000	375.17	0.23*	84.94
17. JHO-897	2.45	-0.09	0.00	0.38	-0.79	0.000	272.41	0.28**	350.17**
18. JHO-995	2.31	-0.63*	0.00	0.30	0.55	0.001**	329.33	0.15*	3370.07**
19. JHO-851E	2.19	0.36	0.04**	0.38	0.98*	0.002**	219.41	-0.12	179.15
20. JHO-99-1	2.25	0.04	0.02*	0.35	0.75	0.001**	328.66	-0.26*	335.60**
21. JHO-99-2	2.23	0.47	0.02*	0.30	-1.49*	0.000	212.33	-0.24*	465.51**
22. JHO-99-3	2.26	0.42	0.00	0.32	0.43	0.000	270.25	-0.05	2227.39**
23. JHO-99-4	2.32	-0.14	0.04**	0.27	-0.05	0.000	227.58	-0.11	2095.96**
24. JHO-99-5	2.10	0.31	0.04**	0.35	-0.50	0.001**	249.00	0.03	1913.85**
25. JHO-99-6	2.57	0.94*	0.05**	0.43	0.65	0.003**	298.08	0.02	-10.60
26. JHO-99-7	2.40	-0.63*	0.00	0.39	-0.28	0.000	324.66	-0.19*	1015.10**
27. Blacknip	2.73	0.33	0.01	0.50	1.54*	0.004**	227.66	0.43**	284.70*
28. S-2688	2.08	-0.22	0.00	0.37	0.73	0.000	271.33	0.70**	500.00**
29. S-3021	2.05	0.04	0.00	0.40	-1.57*	0.007**	269.58	0.57**	518.78**
30. UPO-212	2.24	-0.51	0.00	0.37	1.25*	0.001**	283.33	-0.05	945.89**
31. UPO-230	2.23	-0.06	0.00	0.28	0.34	0.001**	278.00	-0.15*	2943.42**
32. UPO-248	2.20	-0.28	0.01	0.33	-0.19	0.002**	235.83	0.08	1220.02**
33. UPO-250	2.33	-0.33	0.00	0.29	0.24	0.000	255.25	-0.01	710.28**
34. UPO-288	2.10	-1.08**	0.00	0.27	0.48	0.000	247.91	-0.16*	1585.83**
35. OL-661	2.06	-0.11	0.00	0.32	0.24	0.000	272.58	0.37**	1280.52**
36. OL-805	2.01	-0.35	0.00	0.36	0.54	0.008**	287.58	0.21*	68.99
37. OL-936	2.21	-0.01	0.00	0.31	-0.16	0.003**	267.50	0.47**	1184.56**
38. OS-6	2.02	0.04	0.00	0.32	0.55	0.000	242.33	0.02	79.26
39. OS-7	2.65	1.05*	0.01	0.31	-0.21	0.002**	291.00	-0.12	139.65
40. OS-174	2.23	-0.06	0.00	0.34	-0.29	0.001**	290.16	0.04	-47.69
41. OS-189	2.86	-0.30	0.00	0.31	0.65	0.000	356.75	0.41**	51.03
42. OS-237	2.71	0.54	0.00	0.31	0.19	0.000	366.91	0.01	106.13
43. OS-242	2.68	0.17	0.04**	0.29	-0.82	0.003**	331.16	0.27**	254.82*
44. OS-245	2.64	0.90*	0.03**	0.35	0.08	0.003**	254.66	0.20*	-30.95
45. OS-277	2.23	0.97*	0.01	0.34	0.04	0.003**	222.33	-0.10	122.84
46. OS-279	2.02	1.00*	0.00	0.28	-0.22	0.003**	210.75	-0.44**	970.06**
47. OS-285	2.36	0.52	0.02*	0.32	0.02	0.001**	236.50	-0.17*	267.37*
48. OS-286	2.28	0.17	0.00	0.32	-0.79	0.007**	236.58	0.27**	177.85
49. HJ-8	2.91	-0.67*	0.00	0.30	-0.03	0.000	373.41	0.00	135.41
50. HFO-114	2.17	-0.03	0.00	0.32	-1.11*	0.001**	223.83	-0.34**	347.93**
Mean	2.27	0.00	-	0.33	0.00	-	266.69	0.00	-
S.E.	0.08	0.62	-	0.02	0.97	-	16.54	0.13	-

*, ** Significant at P=0.05 and 0.01, respectively

responsiveness, OS-7 exhibited high mean and above average responsiveness and JHO-95-1, JHO-866, JHO-889, JHO-897, Blacknip, OS-189 and OS-237 exhibited high mean and average responsiveness indicating their suitability for poor, good and general environments, respectively.

Leaf: stem ratio:

In case of leaf: stem ratio there were 2 genotypes which had only significant b_i indicating that G x E interactions were linear in nature and performance of these genotypes could be predicted. Significance for both b_i as well as $S^{-2}d_i$, observed for 6 genotypes pointed out that both linear and non-linear type of interactions accounted for the G x E interactions in these genotypes. There were 23 genotypes with significant $S^{-2}d_i$ and as such the performance of these genotypes was not predictable across the environments. Nineteen genotypes indicated absence of G x E interactions when the non-significance of b_i and $S^{-2}d_i$ was considered together (Table 18).

In general, most of the genotypes (42) had b_i approaching to '0'. Only 3 genotypes with $b_i > 0$ and 5 genotypes with $b_i < 0$ showed their suitability for general, favourable and unfavourable environments, respectively. Sixteen genotypes had above average mean, 19 genotypes had average mean and 15 genotypes were below to average mean for leaf: stem ratio. Unstable genotype Blacknip exhibited maximum leaf: stem ratio (0.50; b_i = 1.54*) suggesting its suitability to favourable environments. Genotypes having high mean and response were UPO-212 and JHO-851E, but both these were unstable. JHO-95-2, JHO-897, JHO-99-7 and S-2688 were found stable having high mean performance and showed their adaptability to all kind of environments.

Green fodder yield/plant:

Nine genotypes had non-significant b_i and $S^{-2}d_i$ values indicating the absence of G x E interactions (Table 18). The $S^{-2}d_i$ was

significant for 10 genotypes revealing the presence of non-linear component of G x E interactions and hence prediction of their performance across environments would be difficult. Twenty-three genotypes had both linear and non-linear components of G x E interaction as b_i and $S^{-2}d_i$ values were significant for these genotypes, whereas 8 genotypes had significant bi indicating the presence of linear component.

Out of 50 genotypes, 15 genotypes had $b_i > 0$ value indicating their suitability to favourable environments, another 16 genotypes were having $b_i < 0$ value, which showed their adaptability to unfavourable/poor environments. Remaining 19 genotypes were suitable for general/all kinds of environments as these were having $b_i = 0$. Consideration of mean performance for individual genotypes indicated that 15 genotypes had above average, whereas 20 genotypes were below average and 15 genotypes had average mean performance for green fodder yield per plant. JHO-889 (375.17 g), HJ-8 (373.41 g) and OS-237 (366.91 g) were highest green fodder yielding genotypes. Out of 17 stable genotypes, high mean performance was exhibited by only 9 genotypes. Among them, 4 genotypes JHO-889, JHO-822, OS-189 and OL-805 had above average response and five genotypes, JHO-99-6, OS-7, OS-174, OS-237 and HJ-8 were having average response indicating their adaptability for favourable and general environments, respectively. JHO-851 having below average mean and response showed its suitability to unfavourable environments. However, unstable genotypes for green fodder yield were JHO-96-4 and UPO-212 with $b_i = 0$, JHO-995 and OS-242 with $b_i > 0$ and JHO-99-1 and 99-7 with $b_i < 0$, respectively.

Dry fodder yield/plant:

Simultaneous consideration of two stability parameters b_i and $S^{-2}d_i$ revealed that 6 genotypes showed absence of G x E interactions, as both b_i and $S^{-2}d_i$ were non-significant in their cases (Table 19).

Table 19: Estimates of stability parameters for dry fodder yield/plant, crude protein content and *in vitro* dry matter digestibility in oats

Genotypes	Dry fodder yield/plant (g)			Crude protein content (%)			*In vitro* dry matter digestibility (%)		
	$\bar{X}$	bi	S^{-2} di	$\bar{X}$	bi	S^{-2} di	$\bar{X}$	bi	S^{-2} di
1. Kent	35.25	-0.33**	12.93*	8.67	0.27	0.01	64.54	-0.57*	7.61**
2. DFO-54	57.75	-0.08	11.61*	8.85	-0.41	-0.01	64.38	-0.66*	-0.83
3. DFO-57	54.50	0.22*	1.84	8.55	-0.21	0.04	63.00	-0.88**	-0.48
4. JHO-94-1	34.58	-0.78**	18.08**	9.70	0.37	0.00	67.30	0.77*	4.65*
5. JHO-94-3	47.16	-0.07	8.18	8.63	0.23	0.00	67.05	0.09	-1.11
6. JHO-95-1	60.33	-0.06	11.66*	8.81	0.10	0.09	68.28	0.21	-0.91
7. JHO-95-2	40.25	-0.70**	11.69*	8.73	-0.41	0.27**	67.20	-0.52*	4.41*
8. JHO-96-4	68.33	0.06	41.16**	8.19	-0.32	0.28**	63.58	-0.34	2.07
9. JHO-96-6	49.50	0.07	8.31	8.77	-0.61	0.25**	67.15	0.35	8.33**
10. JHO-97-4	46.16	-0.01	54.09**	9.50	-0.82*	0.89**	69.92	0.29	-0.84
11. JHO-810	35.33	-0.29*	30.40**	8.62	0.78*	-0.02	60.65	-0.52*	-0.50
12. JHO-822	67.00	0.56**	2.02	8.80	-0.73*	0.06	66.35	0.99**	0.28
13. JHO-829	42.33	-0.53**	26.45**	10.08	0.69	0.04	63.57	0.62*	1.31
14. JHO-851	46.91	-0.15*	21.63**	7.77	-0.10	0.16*	61.62	-0.93**	-0.89
15. JHO-866	48.00	-0.42**	32.03**	9.88	1.14*	-0.01	67.04	1.22**	-0.17
16. JHO-889	75.08	0.25*	2.62	9.31	-0.52	-0.02	67.20	-0.32	0.32
17. JHO-897	50.33	-0.18*	110.12**	9.09	-0.43	0.01	66.36	0.12	0.31
18. JHO-995	65.83	0.17*	136.59**	9.10	0.33	0.07	65.34	-0.66*	-0.13
19. JHO-8511	47.00	-0.07	14.81**	8.48	0.06	0.04	62.44	0.29	1.34
20. JHO-99-1	57.83	-0.43**	1.00	8.78	-0.84*	0.07	60.59	0.08	1.82
21. JHO-99-2	40.83	-0.39**	1.51	9.07	0.36	0.32**	62.33	0.66*	-0.17
22. JHO-99-3	57.58	0.00	56.53**	9.20	0.05	-0.01	61.18	-0.45*	-0.88
23. JHO-99-4	50.66	0.13	44.37**	8.78	0.30	-0.01	60.54	-0.57*	0.27
24. JHO-99-5	53.91	0.17*	75.72**	8.64	0.21	0.06	61.21	0.99**	0.63
25. JHO-99-6	54.50	-0.06	6.01	9.45	0.65	0.16*	70.06	0.81**	-0.10
26. JHO-99-7	57.83	-0.37**	36.84**	10.34	-0.08	0.06	71.22	0.69*	-1.08
27. Blacknip	42.50	0.25*	19.57**	11.11	0.96*	0.51**	71.18	0.46*	-0.88
28. S-2688	59.50	0.88**	24.05**	7.96	-1.26*	0.00	63.52	0.18	5.10*
29. S-3021	51.58	0.35**	56.73**	8.04	-0.97*	0.20**	65.31	0.61*	-0.49
30. UPO-212	59.58	0.01	37.42**	9.29	0.98*	0.01	67.76	-0.34	-0.53
31. UPO-230	58.33	-0.09	120.90**	9.47	0.53	-0.01	67.63	-0.75*	0.65
32. UPO-248	49.25	0.19*	31.21**	10.07	0.10	0.47**	69.20	-0.36	0.50
33. UPO-250	52.75	-0.04	16.97**	8.45	-0.14	0.01	62.86	-0.13	0.46
34. UPO-288	54.66	-0.28*	99.03**	8.20	-0.46	-0.01	62.51	-0.37	0.65
35. OI-661	51.66	0.35**	65.22**	9.01	0.34	0.08	61.24	-0.23	0.60
36. OI-805	58.00	0.21*	6.38	8.31	-0.39	0.13*	60.97	0.00	-0.68
37. OI-936	59.83	0.63**	57.68**	8.69	0.09	0.15*	63.57	-0.18	-0.60
38. OS-6	54.08	0.27*	6.02	8.06	-0.34	-0.02	62.53	-0.13	3.32
39. OS-7	61.25	-0.04	7.31	8.20	-0.41	0.07	65.45	-0.29	-0.06
40. OS-174	60.66	0.15*	2.45	8.60	-0.87*	0.10	64.27	-0.05	-0.90
41. OS-189	76.66	0.68**	5.26	8.37	-0.01	0.00	65.14	0.59*	0.57
42. OS-237	71.75	0.12	58.47**	8.60	0.11	-0.01	64.87	0.05	-0.58
43. OS-242	67.75	0.43**	-1.93	8.20	-0.28	0.00	64.65	0.45*	4.70*
44. OS-245	54.33	0.25*	-2.18	8.17	-0.63	-0.01	62.18	-0.32	-0.36
45. OS-277	46.58	-0.03	3.76	8.36	-0.12	-0.02	59.30	-0.47*	-0.84
46. OS-279	47.00	-0.41**	38.68**	8.19	0.00	-0.01	62.96	-0.72*	-1.05
47. OS-285	49.91	-0.26*	22.05**	8.76	-0.09	0.00	58.46	0.26	0.58
48. OS-286	46.33	0.19*	5.45	8.75	0.45	-0.01	63.81	0.89**	0.54
49. HJ-8	79.00	0.07	5.98	10.64	1.06*	0.08	69.45	-0.58*	-0.02
50. HFO-114	36.91	-0.61**	1.18	8.20	1.28*	0.11*	68.62	-0.31	1.90
Mean	53.89	0.00	-	8.87	0.00	-	64.75	0.00	-
S.E.	3.40	0.14	-	0.20	0.71	-	0.79	0.40	-

*, ** Significant at P=0.05 and 0.01, respectively

Eleven genotypes had significant $S^{-2}d_i$ only that showed the presence of non-linear component alone. Twenty genotypes had significant b_i and $S^{-2}d_i$ values which indicated the presence of linear and non-linear components of G x E interactions. Thirteen genotypes had linear component having significant b_i values.

Nineteen genotypes were found stable as these were having non-significant $S^{-2}d_i$. Eighteen genotypes had $b_i > 0$, 15 genotypes $b_i < 0$ and 17 genotypes $b_i = 0$ indicating their suitability to favourable, unfavourable and general environments, respectively. Out of 50 genotypes, 20 genotypes had above average, 10 genotypes average and remaining 20 genotypes were below average in performance for dry fodder yield. Maximum dry fodder yield was recorded in HJ-8 (79.00 g) followed by OS-189 (76.66 g) and JHO-889 (75.08 g). Among stable genotypes, OS-7 and HJ-8 were suited for all types of environments as these were having average response and high mean, whereas JHO-822, JHO-889, OL-805, OS-174, OS-189 and OS-242 had their adaptability to favourable environment as these genotypes were having above average response. JHO-99-1 was below average in response with above average performance showing its potential for poor environments. DFO-57 and OS-245 were found stable and high responsive. However, 11 genotypes exhibited high mean but found unstable. These were DFO-54, JHO-95-1, JHO-96-4, JHO-99-3, UPO-212, UPO-230, OL-936, OS-237, JHO-995, S-2688 and JHO-99-7.

Crude protein content

In case of crude protein content, 29 genotypes indicated absence of G x E interactions when the non-significance of b_i and $S^{-2}d_i$ was considered together (Table 19). The presence of only linear portion of G x E interaction was recorded for 8 genotypes. Four genotypes showed existence of both linear and non-linear portions, whereas for 9 genotypes only non-linear portion was significant.

These results are in close agreement with the information obtained from the combined analysis.

Considering regression coefficient values, 6 genotypes had $b_i > 0$, another 6 genotypes $b_i < 0$, and 38 genotypes $b_i = 0$ indicating their suitability for good, poor and medium environments, respectively. Out of 50 genotypes, 15 genotypes were above average; 13 genotypes were average and 22 genotypes below average in protein content. Blacknip (11.11%) followed by HJ-8 (10.64%) were rich in protein content with above average response (0.96* and 1.06*, respectively) out of which Blacknip was unstable. Other stable and above average protein content containing genotypes were JHO-94-1, JHO-829, JHO-889, JHO-897, JHO-995, JHO-99-3, JHO-99-7 and UPO-230 which showed their adaptability to all types of environments as these were having $b_i = 0$, while HJ-8, JHO-866 and UPO-212 had above average protein content with above average response and stability thus these could be exploited in favourable environments. However, JHO-99-1 and JHO-822 were average in protein content, $b_i < 0$ and stable, which showed their adaptability to unfavourable environments.

***In vitro* dry matter digestibility:**

Simultaneous consideration of both b_i and $S^{-2}d_i$ suggested the absence of G x E interactions in 22 genotypes. Linear component was present for 22 genotypes as shown by significant b_i values (Table 19). In case of 4 genotypes both b_i and $S^{-2}d_i$ were significant indicating that both linear and non-linear components accounted for the total G x E interaction present in case of these genotypes. Non-linear components of G x E interaction were observed for 2 genotypes.

Out of 50 genotypes, 13 genotypes had >0 b_i values indicating their suitability to favourable environments, another 13 genotypes were having <0 b_i values, which showed their adaptability in poor environments. Remaining 24 genotypes were suitable for all type of

environments as these were having b_i values approaching to '0'. Eighteen genotypes had above average mean, 9 genotypes average and 23 genotypes were below average mean performance for this trait. JHO-99-7 and Blacknip had maximum IVDMD content (71.22 and 71.18; b_i =0.69* and 0.46*, respectively). Out of 44 stable genotypes, high mean performance was exhibited by 15 genotypes in which 2 genotypes (HJ-8 and UPO-230) were below average in response, 5 genotypes (Blacknip, JHO-99-7, JHO-822, JHO-866 and JHO-99-6) above average in response and eight genotypes (JH0-94-3, JHO-95-1, JHO-97-4, JHO-889, JHO-897, UPO-212, UPO-248 and HFO-114) average in response which indicate their adaptability for unfavourable, favourable and general environments, respectively.

CHAPTER-V

DISCUSSION

DISCUSSION

Oat, one of the important cereals, is a dual-purpose crop of temperate and sub-tropical areas. Being a highly nutritious cereal, it is equally used for human consumption besides as feed and fodder. Inspite of many beneficial uses, it has so far not received adequate attention from the point of view of genetic improvement and management. Improvement through breeding depends upon the amount of genetic variability available in the gene pool. It is a well known fact that greater the variability among the parents, the greater are the chances of further improvement. The crosses involving diverse parents are expected to greater considerable amount of genetic variability. Moreover, through such crosses the chances of getting transgressive segregants are improved. Therefore, it is necessary to classify the variability available in germplasm and then pick up the parents for hybridization either to exploit heterosis or for getting transgressive segregants (Murty and Pavate, 1962 and Bhatt, 1970). Earlier efforts were mainly confined to the extent of direct selection, which ultimately resulted in the development, and release of numerous high yielding varieties for grain and fodder showing marginal increase in yield. These varieties were found favourable only in the specific agro-climatic conditions in which they were selected and had local adaptability. Genotype x environment interactions are of considerable significance in formulating a breeding programme. The interactions of G x E creates many difficulties in interpreting the results from the experiments conducted in different environments. These interactions often obstruct the rationalization of breeding programmes aimed at improving various crop plants.

Besides being quantitatively better, the forage oats are qualitatively superior as well. Thus, to tap the fodder yielding potential, proper evaluation of genetic material considering different aspects will hopefully constitute the liaison characters between the current and future emphatic areas in improvement and exploitation of forage oats.

Salient features of the results obtained in this study are discussed in the light of the above considerations under the following heads:

5.1 Genetic variability

5.2 Genetic divergence

5.3 Correlation and path-coefficient analysis

5.4 Stability analysis

5.1 GENETIC VARIABILITY

Ample variation among 50 genotypes for all the traits indicated its significance for estimation of further parameters of variation in the material studied.

Considering mean performance of genotypes, the timely sown environments (E_1 and E_3) were found better than the late sown environments (E_2 and E_4) for fodder yield and most of the component traits. Early flowering was observed in E_2. Wide range of variation was observed in E_1 followed by that in the E_3, whereas it was minimum in E_2 and E_4 for fodder yield and yield contributing traits. High green and dry fodder yielding genotypes over the four environments were HJ-8, JHO-96-4, JHO-822, JHO-889, JHO-995, JHO-99-1, OS-7, OS-174, OS-189, OS-237 and OS-242. These genotypes were having more than 10 per cent superiority over the grand mean of green and dry fodder yield per plant. From the above, it can be suggested that the above genotypes can be selected and used as one of the parents in hybridization programme.

Any selection programme mainly depends on the extent and nature of genetic variability present and on also the genetic architecture of yield and the component characters with high heritability as it is likely to give high genetic advance provided the traits are direct components of yield. High genotypic coefficient of variance was observed for the various traits like green and dry fodder yield per plant, number of leaves per plant and number of tillers per plant. There was a close relationship between phenotypic and genotypic coefficient of variation in almost all the characters in all the environments. However, phenotypic coefficients of variation were slightly higher than their corresponding genotypic coefficient of variation. It was obvious that the selection of better genotypes could be done based on their phenotype. The studies of Singh and Katoch (1975), Bhagmal *et al.* (1975), Nair and Gupta (1977), Choubey and Gupta (1986), Rahaman and Roquib (1987), Bahl *et al.* (1989), Kumar *et al.* (1995), Hosoya *et al.* (1998), Singh (1999) and Nehvi Shafiq *et al.* (2000) indicated presence of enough variability for various traits in oats confirming to the results of the present study. However, Swarup and Chaugale (1962) suggested that genetic coefficient of variation alone is not sufficient for determination of the amount of heritable variation and hence heritability in conjunction with genetic advance is required to be studied. Burton and Devane (1953) also suggested that genetic coefficient of variability together with the heritability estimates would give reliable indication of the expected amount of improvement by selection.

Panse (1957) expressed that high heritability together with high genetic advance was an indicative of additive gene effects and high heritability associated with low genetic advance was indication of dominance and epistatic effects. In the present study, high heritability coupled with high genetic advance was observed for plant height,

number of tillers per plant, stem diameter, number of leaves per plant, leaf length, leaf breadth, leaf: stem ratio, green and dry fodder yield per plant in all the environments. This indicated that in these traits improvement could be made by simple selection. These results are in conformity with those of Bhagmal *et al.* (1975), Nair and Gupta (1977), Choubey and Gupta (1986), Bahl *et al.* (1989), Srivastava *et al.* (1995), Singh (1999) and Nehvi Shafiq *et al.* (2000). In contrast to present results, Rahaman and Roquib (1987) reported low heritability estimates for green and dry fodder yield, leaf breadth and number of tillers per plant, while Singh and Katoch (1975) reported low genetic advance for green fodder yield. The variation in the findings of different workers could be ascribed to differences in environment and also due to material used. Although, the traits were having high heritability estimates but magnitude of genetic advance was low indicating thereby the presence of dominance and epistatic gene effects. Johnson *et al.* (1955) also reported that higher estimates of heritability not to be associated with higher genetic values of genetic advance.

5.2 GENETIC DIVERGENCE

Classification of genetic diversity in the germplasm has special significance because of two specific reasons. First, it is difficult to evaluate large number of lines in breeding programmes obviously due to practical limitations and second because many of the accessions may be genetically more or less similar due to common ancestor.

Various approaches like geographical diversity (Dhawan and Singh, 1961; Moll *et al.*, 1962; Singh and Joshi, 1966), coefficient of racial likeness (Pearson, 1926), discriminant function (Fisher, 1936), metroglyph and index score analysis (Anderson, 1957) have been suggested for classification and selection considering many variables simultaneously. But these failed to provide foolproof measure of genetic

diversity and its quantitative assessment. D^2 statistics of Mahalanobis (1930, 1936), a measure of group distance based on multiple characters permits precise quantitative comparison among all pairs of population along with their classification. D^2 analysis is based on second degree statistics and is self-weighing on the basis of genetic variability of characters involved. Also the D^2 value between any pair of populations amounts to the measure of genetic divergence (Rao, 1952).

In the present study, the estimates of D^2 values revealed wide range of diversity among the genotypes. This was further substantiated by the grouping pattern of the genotypes. The 50 genotypes under study were grouped into 8 clusters (E_1 and E_2), 9 clusters (E_3 and E_4), whereas in pooled analysis, ten clusters were formed with the I cluster having the maximum number of genotypes followed by cluster II in all the environments. This envisaged that the genotypes grouped within a particular cluster are more or less genetically similar to each other and apparent wide diversity is mainly due to the remaining genotypes distributed over rest of the other clusters in various environments (7 E_1 and E_2; 8 E_3 and E_4; 9 pooled, respectively). Clustering pattern of genotypes in this study revealed that genotypes from different geographic regions are grouped together in a cluster and *vice-versa* suggesting that the geographical diversity does not necessarily represent genetic diversity as has also been reported by Sidhu and Mehndiratta (1981), Pukhal' Skii *et al.* (1990), Bedis and Patil (1993), Kishor *et al.* (1996), Babbar *et al.* (1997) and Choubey *et al.* (2001) in oats. Thus, geographical diversity although important, was not the only factor responsible in determining the genetic diversity. The grouping of genotypes originating from different eco-geographical regions into one cluster could be attributed to frequent exchange of breeding material and due to operation of similar forces of natural and artificial selection

resulting in perpetuation and stabilization of similar genotypes (Murty and Arunachalam, 1966).

The main objective of forming clusters and to find out the intra and inter-cluster distances is to provide relevant information for selection of diverse parents for hybridization programme without making actual crosses (Bhatt, 1970). The lesser magnitude of intra-cluster distances than those of inter-cluster distances indicated that the genotypes grouped in a common cluster diverged very little from one another as compared to the genotypes of different cluster. Large inter-cluster distances signify that the genotypes grouped in a cluster are different from the genotypes of other clusters for one or more characters, which made them so divergent from others.

The cluster means reflected appreciable variation for almost all the characters among different clusters in different environments. These differences were more pronounced for green and dry fodder yield potential. In forage oats, Nair and Gupta (1977), Kishor *et al.* (1996), Bedis and Patil (1993) and Choubey *et al.* (2001), while studying different germplasm accessions using D^2 analysis reported grouping of different genotypes in various clusters. The single genotype clusters represented genotypes having mostly inferior characteristics yet were found to have accumulated a few good attributes in them which could be desirable for forage oat breeding programme.

Results obtained from this study indicated that the actual D^2 values among the genotypes rather than inter-cluster D^2 values should also be considered because the clustering pattern on the basis of D^2 statistic is totally arbitrary. The hybridization among diverse parents is likely to produce heterotic hybrids and desirable transgressive segregants in further generations and hence the genotypes with better mean values should be used for the success in the breeding programmes.

Rana and Murty (1971), Sindhu and Singh (1975) and Singh and Gupta (1979) reported the classification according to D^2 analysis as subjective, firstly because of the cluster formation method, secondly, sometimes genetically related genotypes may be grouped into different clusters and *vice-versa* and thirdly, the number and composition of clusters varies greatly under the influence of environments. Therefore, they suggested that in the absence of more precise method, it becomes necessary to use more than one method to offset these limitations to a certain extent. Romeshburg (1990) opined that findings of similar alternatives reduce the decision problem to two stages i.e. first, to select the cluster that can best achieve the planning objective, and second select the best alternate within the best cluster.

5.3 CORRELATION AND PATH-COEFFICIENT ANALYSIS

Fodder yield, being a complex character, is the cumulative and interactive effect of a number of component traits. Direct selection for yield *per se* generally results in low genetic gain because of its low heritability in general dictating plant breeders to realize the importance of component traits. However, because of their complex interactive nature with each other, information on association of these component traits with yield and among themselves is of utmost importance. Grafius (1959) strongly advocated the use of component breeding approach in order to achieve further improvement in yield. Correlation between the characters could be due to linkage, pleiotrophy or developmental factors. Correlation due to linkage could be broken through recombination but the later may not be easily controlled without bringing improvement in component characters. The correlations due to developmental causes were what gave rise to the idea of yield component compensation and the comment, "man can arrange independent gene systems, but the plant rearranges the combined

results" (Grafius *et al.*, 1976). The inclusion of all the characters in selection programme is obviously not practicable and under these situations correlation and path-coefficient analysis are quite useful in formulating an effective and efficient selection programme.

The present study revealed that genotypic correlations, in general, were of higher magnitude as compared to their corresponding phenotypic correlations in all the environments in most of the character combinations. This indicated that environments played a backward role in determining phenotypic correlations that is why, the phenotypic correlations are generally less than genotypic correlations. Green fodder yield was found to be positively and significantly correlated with plant height, stem diameter, number of leaves per plant, leaf length, leaf breadth and dry fodder yield per plant, while days to 50 per cent flowering, number of tillers per plant, protein content and IVDMD (except E_2 and E_3) had positive correlation only with green fodder yield. However, leaf: stem ratio had positive correlation with green fodder yield in two environments (E_1, E_3) and negative in other environments (E_2, E_4). This was in consonance with the findings of Bhagmal *et al.* (1975), Singh and Katoch (1975), Dhumale and Mishra (1979), Choubey and Gupta (1986), Bahl *et al.* (1988), Dubey *et al.* (1995), Srivastava *et al* (1995), Singh and Nanda (1998), Nehvi Shafiq *et al.* (2000) and Choubey *et al.* (2001) in oat.

Often, many of the characters are correlated because of a mutual association, positive or negative, with other characters. As more variables are considered in the correlations the direct associations become more complex, less obvious and somewhat perplexing. At this point, the path-coefficient analysis provides an effective means of separating direct and indirect causes of association and permits critical

examination of the specific forces acting to produce a given correlation and measures the relative importance of each casual factor.

It is obvious from the gist of results of path-coefficients analysis (Table 20) that number of leaves per plant, leaf breadth, plant height, stem diameter, leaf length and number of tillers per plant were the component traits of green fodder yield as these had high values of direct effects. But all these characters also had large positive indirect effects on green fodder yield through each other. Almost similar trend of results of path-coefficient analysis was observed in case of dry matter yield. These results are in conformity with the findings of Dhumale and Mishra (1979), Choubey and Gupta (1986), Bahl *et al.* (1988), Srivastava *et al.* (1995) and Nehvi Shafiq *et al.* (2000).

Table 20: Direct and indirect effects of various traits on green fodder yield in oats in descending order

E_1	E_2	E_3	E_4	Pooled
0.3928, SD	**0.5521, PH**	**0.7771, NL**	**0.6252, NL**	**0.5332, SD**
0.1546, PH	0.1084, LB	0.0254, LB	0.0253, LL	0.2901, PH
0.3394, NT	**0.2746, LB**	**0.4908, LB**	**0.6220, PH**	**0.4804, PH**
0.1165, NL	0.2179, PH	0.0517, PH	0.0961, SD	0.3221, SD
0.2504, PH	**0.2728, NL**	**0.2029, LL**	**0.2936, SD**	**0.3577, NL**
0.2426, SD	0.1303, NT	0.0858, PH	0.2036, PH	0.1154, NT
0.1512, NL	**0.1597, NT**	**0.0934, PH**	**0.0311, 50% F**	**0.1383, NT**
0.2614, NT	0.2226, NL	0.2715, LB	0.0802, SD	0.2984, NL
0.1139, LL	**0.1116, SD**	**0.0020, 50% F**	**0.0075, NT**	**0.0935, LL**
0.2191, SD	0.2803, PH	0.0776, NL	0.5670, NL	0.2742, PH
0.1131, LB	**-0.0270, 50% F**	**-0.0058, SD**	**-0.0081, LB**	**-0.0923, LB**
0.3142, SD	0.1184, PH	0.4230, LB	0.3592, PH	0.4806, SD
-0.0066, 50% F	**-0.0412, LL**	**-0.1674, NT**	**-0.0808, LL**	**-0.0932, 50% F**
0.0529, SD	0.3120, PH	0.6744, NL	0.4247, PH	0.1810, SD
-0.0796, LSR	**-0.1287, LSR**	**-0.4170, LSR**	**-0.1669, LSR**	**-0.1010, LSR**
0.0718, NT	0.1071, NL	0.2939, NL	0.1930, NL	0.1695 NL

Values in **bold** letters represent direct effects.
50% F= Days to 50% flowering; PH= Plant height, NT= No. of tillers/plant, NL= No. of leaves/plant, SD= Stem diameter, LL= Leaf length, LB= Leaf breadth, LSR= Leaf: stem ratio

The multitude of component characters, their positive and negative effects with one another and fodder yield along with environmental interactions make the prediction and determination of high fodder yielding genotypes extremely difficult. Hence, the selection should only be based on above mentioned component traits for faster genetic amelioration of fodder yield in oat.

In the light of results obtained in the present investigation, it is clear that plant height, stem diameter, number of leaves per plant, leaf length and leaf breadth are comparatively more important component characters for green as well as of dry fodder yield. Therefore, an ideal plant type in oat can be described as one, which is characterized by tall nature with profuse tillering, more leaf number, leaf length and breadth and more stem diameter. The improvement and selection based on these traits would also result not only in increased in green and dry fodder yield but also quality.

5.4 STABILITY ANALYSIS

From the work of Yates and Cochran (1938), Finlay and Wilkinson (1963), Eberhart and Russell (1966), Bucio-Alanis (1966), Bucio-Alanis and Hill (1966), Perkins and Jinks (1968 a,b), Breese (1969) and Freeman and Perkins (1971), the most important conclusion which has emerged out is that the bulk of genotype x environment interaction is often a linear function of the environmental means, although both linear and non-linear function played an important role in building up of the total genotype x environment interactions. The range of genotypes could provide an efficient tool to measure and grade a series of environments. In order to get the unbiased estimates of stability parameters, the genotypes must be grown in adequate number of environments covering the range of environmental conditions (Eberhart and Russell, 1966). The joint regression analysis of Perkins

and Jinks (1968 a), followed in the present investigation, bridges the gap between the statistical and genetical approaches and provides better genetic interpretation of the results obtained.

Considerable genetic variability existed among the genotypes for various traits and the environments where the studies were conducted varied markedly for better expression of all the characters. The significant mean squares due to G x E interactions indicated that genotypes showed differential response to the change in environmental conditions. Occurrence of such interactions has also been reported by several other workers in oats (Paroda *et al.*, 1973; Kumar *et al.*, 1982; Singh *et al.*, 1984; Thaware, *et al.*, 1992; Singh *et al.*, 1992; Gupta and Singh, 1997; Babbar *et al.*, 1998; Pundir *et al.*, 2002).

It was further noticed that both linear and non-linear components significantly contributed to the total G x E interaction for all the characters. However, relative magnitude of both these portions varied with the characters (Table 14). There was preponderance of linear components for days to 50 per cent flowering, plant height, number of tillers per plant, number of leaves per plant, green and dry fodder yield per plant and IVDMD and hence G x E interaction for these characters could be predicted reliably based on linear regression which had considerable practical value. The magnitude of non-linear component of G x E was observed for stem diameter, leaf length, leaf breadth, leaf: stem ratio and protein content. This showed that complex relationship existed between the genotypes and environmental effects and the prediction of genotypes for these characters could not be made easily when both the heterogeneity between regression (linear) and remainder (non-linear) are significant. However, the predictions will be more reliable only when heterogeneity between regression (linear) is significant (Breese, 1969).

The environmental index values revealed that E_1 was the best environment for expression of all the characters, whereas E_3 was best for plant height, stem diameter, leaf length, leaf breadth, crude protein content and IVDMD. However, E_2 and E_4 were poor environments for most of the traits except for earliness.

In the model proposed by Perkins and Jinks (1968a), linear regression coefficient (b_i) accounts for linear component of G x E interaction and is a convenient measure of response of a genotype to change in the environment. A genotype, which is above average response, has b_i value significantly greater than zero, such a genotype is useful for favourable environments. In contrast, a genotype, which has bi value significantly less than zero, such a genotype is useful for poor/ unfavourable environments. A genotype which is relatively indifferent to the variation in the environment is said to be average responsive and will have bi value not significantly different from zero, such a genotype is useful to general/all kinds of environments.

Originally, Finlay and Wilkinson (1963) used the term 'stability' to refer the slope of the regression lines. Genotypes with the most gentle slopes being the most stable in contrast to the genotypes having the steepest slopes, which were the least stable. It has also been recognized that the slope measures the response of the genotype to a change in environment and would perhaps be better referred to as 'responsiveness'. Further, 'stability' should be used to refer the absence or low deviation from regression, which measure the responsiveness of the genotype in different environments (Breese, 1969; Samuel *et al.*, 1970). A stable variety, under this concept would be one whose performance could be predicted easily and precisely. This definition of stability would be same as Perkins and Jinks (1968 a). Thus, the

genotype with smallest amount of deviation around the regression line is considered to be most stable.

The important practical aspect is the existence of G x E interaction, the major portion of which is linear. When there is no G x E interaction or where such interactions are linear, the behaviour of such genotypes are predictable across the environments. But, such predictions become impossible, if non-linear component of G x E interactions are predominant. In the present study, similar situation emerged when one considers the proportion of variance due to linear portion (heterogeneity between regression) and non-linear portion (remainder) of G x E interaction in joint regression analysis. More than 50 per cent variance of G x E interaction could be accounted due to linearity for days to 50 per cent flowering, plant height, number of tillers per plant, number of leaves per plant, green and dry fodder yield per plant and IVDMD, whereas stem diameter, leaf length, leaf breadth, leaf: stem ratio and protein content accounted for non-linear component (Table 21).

Table 21: Magnitude (%) of linear and non-linear components of G x E interaction for different characters in oats

	Characters	Linear	Non-linear
1.	Days to 50% flowering	51.80	48.20
2.	Plant height (cm)	56.76	43.24
3.	Number of tillers/plant	65.71	34.29
4.	Stem diameter (mm)	43.76	56.24
5.	Number of leaves/plant	66.48	33.52
6.	Leaf length (cm)	40.37	59.63
7.	Leaf breadth (cm)	38.24	61.76
8.	Leaf: stem ratio	37.04	62.96
9.	Green fodder yield/plant (g)	83.81	16.19
10.	Dry fodder yield/plant (g)	85.75	14.25
11.	Crude protein content (%)	39.41	60.59
12.	*In vitro* dry matter digestibility (%)	64.56	35.44

In the studies of many workers, it has been revealed that even for the unpredictable characters, prediction can still be made when one considers stability parameters of individual genotypes. In the present study, same situation was found when stability parameters of individual genotypes were considered (Table 22). From this table, the performance of majority of the genotypes was predictable in respect of leaf breadth, protein content and IVDMD. This discrepancy might be due to the differential testing procedures in the two analyses. However, days to 50% flowering, plant height, number of tillers per plant, stem diameter, number of leaves per plant, leaf length, leaf: stem ratio, green and dry fodder yield per plant exhibited unpredictable behaviour (Table 22).

Table 22: Distribution of different genotypes on the basis of different stability parameters for various characters in oats

Characters	Predictable		Unpredictable	
	Both bi and $S^{-2}di$ non-significant	Only bi significant	Both bi and $S^{-2}di$ significant	Only $S^{-2}di$ significant
1. Days to 50% flowering	5	3	14	28
2. Plant height (cm)	7	3	15	25
3. Number of tillers/plant	12	11	9	18
4. Stem diameter (mm)	15	6	6	23
5. Number of leaves/plant	8	9	13	20
6. Leaf length (cm)	12	1	10	27
7. Leaf breadth (cm)	27	8	2	13
8. Leaf: stem ratio	19	2	6	23
9. Green fodder yield/plant(g)	9	8	23	10
10. Dry fodder yield/ plant (g)	6	13	20	11
11. Crude protein content (%)	29	8	4	9
12. IVDMD (%)	22	22	4	2

Nearly, 34 per cent and 38 per cent of the genotypes showed predictable behaviour for green and dry fodder yield per plant, respectively. These results are in close agreement with the findings of Paroda *et al.* (1973), Kumar *et al.* (1982), Singh *et al.* (1984), Thaware *et al.* (1992), Singh *et al.* (1992), Kishor *et al.* (1994), Gupta and Singh (1997), Babbar *et al.* (1998) and Pundir *et al.* (2002), whereas Prakash *et al.* (1989) and

Prakash and Kishor (1990) reported the results in contradiction to the results of present study.

The present study helped to identify some genotypes, which could be suitable for different kinds of environmental conditions. The selected genotypes are likely to give predicted response for green and dry fodder yield in a given environment. According to Perkins and Jinks (1968a), a desirable variety is one, which has high mean ($\bar{X}$) with b_i and $S^{-2}d_i$ values approaching to zero.

The genotypes were grouped on the basis of the results of three stability parameters. Out of 50, none of the genotype was found to be stable for all the 12 characters studied. Hence, a comparative statement for stability parameters was made to sort out some promising high yielding stable genotypes with respect to fodder yield and quality traits components (Table 23).

Table 23: Directory of promising genotypes with respect to stability parameters for fodder yield and quality traits in oats

Characters	Stability parameters	Genotypes										
		JHO-95-1	JHO-822	JHO-889	JHO-99-6	OL-805	OS-7	OS-174	OS-189	OS-237	OS-242	HJ-8
Green fodder yield/plant(g)	M	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA
	R	A	AA	AA	A	AA	A	A	AA	A	AA	A
	S	S	S	S	S	S	S	S	S	S	US	S
Dry fodder yield/plant(g)	M	AA	AA	AA	A	AA	AA	AA	AA	AA	AA	AA
	R	A	AA	AA	A	AA	A	AA	AA	A	AA	A
	S	US	S	S	S	S	S	S	S	US	S	S
Crude protein content (%)	M	A	A	AA	AA	BA	BA	BA	BA	BA	BA	AA
	R	A	BA	A	A	A	A	BA	A	A	A	AA
	S	S	S	S	US	US	S	S	S	S	S	S
IVDMD (%)	M	AA	AA	AA	AA	BA	A	A	A	A	A	AA
	R	A	AA	A	AA	A	A	A	AA	A	AA	BA
	S	S	S	S	S	S	S	S	S	S	US	S

M=Mean; R=Response; S=Stable; US=Unstable; A=Average; AA=Above average; BA=Below average

In the present study, genotypes, JHO-822, JHO-889, OL-805, OS-189, OS-7, OS-174 and HJ-8 were found stable and high yielder for

green as well as dry fodder yield, while JHO-95-1, JHO-99-6 and OS-237 possessed high green fodder yield. However, OS-242 had above average dry fodder yield. Out of stable and high fodder yielding genotypes, HJ-8, JHO-889 and JHO-822 were found rich in protein content and better in digestibility. Based on all this, it is suggested that above mentioned genotypes may be exploited in future breeding programme in order to improve the fodder yield and quality in oat.

For identifying the parental genotypes to be included in a broad based hybridization programme, not only the genetic divergence among them but also their stability needs to be considered. In this background, an attempt was made to identify such genotypes in the present study (Table 24).

Table 24: Promising genotypes selected for hybridization based on genetic divergence and stability in oats

	Genotypes	Major features
1.	JHO-95-1	Most divergent, stable, tall, broad leaves, high fodder yielding, better IVDMD
2.	JHO-822	Most divergent, stable, extra-early, profuse tillering, more leaves, high fodder yielding, high protein, better IVDMD
3.	JHO-889	Most divergent, stable, very tall, profuse tillering, more stem diameter and leaves, broad leaves, high fodder yielding, high protein, better IVDMD
4.	HJ-8	Divergent, stable, very tall, more stem diameter, long and broad leaves, high fodder yielding, high protein, better IVDMD
5.	OS-189	Divergent, stable, tall, more stem diameter, long and broad leaves, high fodder yielding
6.	JHO-99-6	Divergent, stable, tall, more stem diameter, long and broad leaves, high protein, better IVDMD
7.	OS-174	Divergent, stable, tall, long leaves, high fodder yielding
8.	OL-805	Divergent, stable, medium height, long leaves, high fodder yielding
9.	OS-7	Most divergent, stable, tall, more stem diameter, broad leaves, high fodder yielding
10.	OS-237	Divergent, stable, early, tall, more stem diameter, long and broad leaves, high fodder yielding

Genetic divergence (selecting them from different clusters) and stability were considered simultaneously for green and dry fodder yield in this attempt. A few other traits were also considered. On this basis, the genotypes JHO-95-1, JHO-822, JHO-889, OS-189, HJ-8, JHO-99-6, OS-174, OL-805, OS-7 and OS-237 were found most promising for hybridization in the present material. Best approach would be to cross them in a diallel fashion and exploit the segregating generations. Alternatively, paired crosses, followed by double crosses can also be employed. In that case, their number has to be reduced further. This approach can possibly be confined only to the first 4 or 6 genotypes because of limitations in producing double crosses.

CHAPTER-VI

SUMMARY

SUMMARY

The experimental material of 50 diverse genotypes of forage oats (*Avena sativa* L.) was evaluated at the research area of the Division of Crop Improvement, Indian Grassland and Fodder Research Institute, Jhansi and Forage Research Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar under normal and late sown conditions during the *rabi* season of 1999-2000, thereby comprising four environments in all. Each genotype was planted in a randomized block design replicated thrice in two rows of 4 m length spaced 30 cm between rows and 10 cm between plants. The observations on five randomly selected plants from each genotype in each replication in each environment were recorded for days to 50% flowering, plant height (cm), number of tillers per plant, stem diameter (mm), number of leaves per plant, leaf length (cm), leaf breadth (cm), leaf: stem ratio, green and dry fodder yield per plant (g), crude protein content (%) and *in vitro* dry matter digestibility (%). The data of four environments were pooled after conducting the Bartlett's test and subjected to estimate the genetic variability components, genetic divergence, associations, path-coefficient analysis and phenotypic stability of various fodder yield and quality traits. The salient findings of this study are summarized as under:

1. Significant differences for various traits in all the environments indicated that ample variability existed among the genotypes.
2. An adequate variability was observed for various traits and estimates of genotypic and phenotypic coefficients of variation were quite close to each other, suggesting little role of environment. The estimates of heritability were high for all the characters, whereas moderate to high genetic advance was observed for all the characters. High heritability

coupled with high genetic advance was observed for most of the traits, particularly green and dry fodder yield per plant.

3. The analysis of genetic divergence through Mahalanobis D^2 statistics revealed considerable genetic diversity among genotypes. The genotypes were grouped into 8 homogenous clusters in E_1 and E_2, 9 in E_3 and E_4 and 10 in pooled basis. Cluster I composed of maximum 13, 14, 14, 16 and 11 genotypes followed by Cluster II having 8, 12, 8, 9 and 10 genotypes in E_1, E_2, E_3, E_4 and pooled basis, respectively, whereas Cluster VIII (E_1, E_2), IX (E_3, E_4) and X (pooled basis) contained a single genotype. No correspondence was observed between the geographical and genetic diversity in all the environments.
4. The intra-cluster distances were relatively smaller than inter-cluster distances indicating homogenous nature of groups and presence of narrow genetic variation within a cluster in all the environments. The maximum inter-cluster distance was observed between cluster III and V followed by V and VII, III and IV and I and V; between clusters V and VII followed by VI and VII, IV and VII and III and VIII; between clusters V and VII followed by VII and IX, III and VII and V and VI; between clusters II and IV followed by IV and VIII, II and VI and II and V; between clusters IX and X followed by I and X, IV and X and III and IX in E_1, E_2, E_3, E_4 and pooled basis, respectively. The use of genotypes in hybridization from these clusters having most of the desirable characters is likely to produce more transgressive segregants. The D^2 analysis further indicated that high variation for various fodder yield contributing traits had maximum contribution towards genetic divergence.
5. In general, genotypic correlation coefficients were found to be higher than their corresponding phenotypic correlation coefficients. Green and dry fodder yield per plant was found to be positive and significantly

correlated with plant height, stem diameter, number of leaves per plant, leaf length and leaf breadth in all the environments.

6. Path-coefficient analysis further confirmed that the characters such as plant height, stem diameter, number of tillers and leaves per plant, leaf length and leaf breadth were the major component traits of green and dry fodder yield and hence these should be given priority in selection in view of their high heritability coupled with high genetic advance also.
7. The joint regression analysis indicated significant differences among the genotypes for all the characters. The environments of experimentation also differed significantly. The G x E interaction and its two components viz., heterogeneity between regression and remainder were significant for all the traits indicating importance of both linear and non-linear components of G x E interaction. There was preponderance of linear components for days to 50% flowering, plant height, number of tillers per plant, number of leaves per plant, green fodder yield per plant, dry fodder yield per plant and IVDMD and hence prediction of genotypes appeared possible for these traits. However, non-linear components of G x E interaction was higher than linear components for stem diameter, leaf length, leaf breadth, leaf: stem ratio and crude protein content indicating that prediction could not be made easily for these characters.
8. Based on environmental index, E_1 was the best and most favourable environment for all the characters. E_2 was good for number of tillers and leaves per plant and leaf: stem ratio, E_3 for days to 50% flowering, plant height, stem diameter, leaf length, leaf breadth, crude protein content and IVDMD. However, E_4 was the poorest for most of the characters except days to 50% flowering and leaf: stem ratio. Performance of genotypes for different characters in normal sown environments (E_1 and E_3) was better than that of late sown environments (E_2 and E_4).

9. The estimation of stability parameters for individual genotypes indicated that the proportion of genotypes exhibiting predictable behaviour was more for leaf breadth, crude protein content and IVDMD.
10. The genotypes JHO-822, JHO-889, OL-805, OS-189, OS-7, OS-174, and HJ-8 were found stable and high yielding for both green and dry fodder yield. As far as yield and quality is concerned, the genotypes HJ-8, JHO-889 and JHO-822 were found stable and high in crude protein content and better in digestibility.
11. Considering both genetic divergence and phenotypic stability together, the selected genotypes can be used as promising parents for hybridization. The most promising genotypes selected include: JHO-95-1, JHO-822, JHO-889, OS-189, HJ-8, JHO-99-6, OS-174, OL-805, OS-7 and OS-237.

Thus, the present study was a successful attempt in identifying the elite genotypes based on genetic divergence, genetic variability, stability, their performance and the understanding of complex interrelationship among attributes involved in genetic control of fodder yield and quality of oat. Therefore, these results will provide valuable added guidelines in future breeding programmes for improving the fodder yield and related traits as per the need of this crop in order to enhance over all quality forage production in the country.

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APPENDIX

APPENDIX

Mean performance of different genotypes for various characters in oats

Sr. No.	Genotypes	Days to 50% flowering					Plant height (cm)				
		E_1	E_2	E_3	E_4	Pooled	E_1	E_2	E_3	E_4	Pooled
1	Kent	96.00	87.00	121.00	106.00	102.50	110.33	87.33	97.33	93.67	97.16
2	DFO-54	103.33	77.33	120.00	99.00	99.91	121.67	90.67	118.33	113.00	110.91
3	DFO-57	104.33	74.66	115.33	101.00	98.83	102.33	96.33	106.00	93.33	99.50
4	JHO-94-1	106.67	80.00	117.00	100.33	101.00	92.67	76.33	100.67	86.00	88.91
5	JHO-94-3	106.67	88.00	125.00	107.67	106.83	108.00	104.00	119.67	107.00	109.66
6	JHO-95-1	112.00	91.00	127.67	112.00	110.67	131.67	122.00	127.67	104.67	121.50
7	JHO-95-2	113.00	88.00	131.00	109.67	110.41	105.67	98.67	102.33	93.00	99.91
8	JHO-96-4	111.00	89.00	117.00	109.00	106.50	121.67	104.33	125.00	105.00	114.00
9	JHO-96-6	110.67	91.00	127.00	111.00	109.91	103.33	95.00	108.00	88.33	98.66
10	JHO-97-4	115.00	84.00	130.00	109.67	109.75	101.67	90.67	97.67	82.67	93.16
11	JHO-810	116.00	81.00	118.00	107.67	105.66	91.67	85.00	89.00	78.33	86.00
12	JHO-822	106.66	78.33	111.00	105.00	100.25	97.33	93.33	96.33	86.33	93.33
13	JHO-829	103.00	75.33	121.00	103.67	100.75	94.33	84.67	110.67	92.00	95.41
14	JHO-851	108.00	85.00	128.33	111.00	108.08	106.00	91.33	104.33	90.00	97.91
15	JHO-866	125.00	89.00	126.00	112.66	113.16	101.33	92.33	111.00	94.67	99.83
16	JHO-889	114.00	89.67	127.00	109.33	110.00	128.33	120.67	128.67	121.33	124.75
17	JHO-897	113.33	84.66	127.66	112.00	109.41	111.00	102.00	98.00	88.00	99.75
18	JHO-995	114.33	89.33	125.00	109.66	109.58	107.33	100.67	129.33	99.67	109.25
19	JHO-851E	117.66	86.00	126.33	110.66	110.16	114.67	98.00	112.67	94.33	104.91
20	JHO-99-1	117.66	84.00	110.00	111.00	105.66	115.67	107.33	123.67	101.33	112.00
21	JHO-99-2	110.66	83.67	110.00	108.00	103.08	106.67	107.00	99.00	89.33	100.50
22	JHO-99-3	108.00	93.33	123.33	109.66	108.58	126.33	116.33	127.67	106.67	119.25
23	JHO-99-4	112.00	86.66	125.00	109.66	108.33	112.33	100.67	118.33	102.33	108.41
24	JHO-99-5	112.33	86.00	121.00	108.00	106.83	116.33	93.00	110.00	91.33	102.66
25	JHO-99-6	115.00	87.00	130.00	102.00	108.50	123.00	95.00	128.00	110.00	114.00
26	JHO-99-7	119.00	81.00	125.33	106.67	108.00	97.33	100.33	103.67	91.00	98.08
27	Blacknip	116.66	83.33	127.00	120.67	111.91	100.66	74.00	93.33	68.70	84.16
28	S-2688	101.33	92.00	126.33	109.00	107.16	98.33	92.67	110.00	100.33	100.33
29	S-3021	106.00	91.00	131.00	111.33	109.83	111.33	102.00	107.00	85.67	101.50
30	UPO-212	118.00	80.33	119.33	107.66	106.33	119.33	113.00	113.33	110.33	114.00
31	UPO-230	111.00	80.00	127.00	105.67	105.91	117.33	118.67	119.33	108.00	115.83
32	UPO-248	108.33	87.00	130.33	110.33	109.00	135.33	92.67	123.67	105.33	114.25
33	UPO-250	112.33	74.00	113.00	105.00	101.08	121.33	102.67	112.66	105.67	110.58
34	UPO-288	104.00	82.33	111.00	97.66	98.75	101.67	108.33	98.33	104.00	103.08
35	OL-661	116.00	81.33	125.33	108.33	107.75	119.00	98.67	121.33	96.00	108.75
36	OL-805	112.33	88.00	126.00	111.00	109.33	115.00	109.33	117.00	99.33	110.16
37	OL-936	112.00	90.00	125.00	109.00	109.00	126.33	86.00	126.67	108.00	111.75
38	OS-6	109.66	90.33	117.00	105.66	105.66	104.33	97.00	113.67	98.00	103.25
39	OS-7	110.33	91.00	119.00	108.33	107.16	130.00	100.00	127.00	115.33	118.08
40	OS-174	107.66	83.00	121.00	109.00	105.16	105.67	120.67	116.00	103.67	111.50
41	OS-189	105.66	83.33	127.33	109.66	106.50	140.33	113.33	142.33	122.33	129.58
42	OS-237	111.00	86.33	124.66	112.00	108.50	128.67	123.33	144.33	120.00	129.08
43	OS-242	114.33	91.33	125.66	112.66	111.00	130.33	116.00	140.67	115.00	125.50
44	OS-245	104.00	91.66	122.00	109.33	106.75	134.33	114.33	136.67	123.67	127.25
45	OS-277	108.00	83.66	121.00	105.00	104.41	105.00	101.00	110.00	97.33	103.33
46	OS-279	106.33	88.00	122.00	106.00	105.58	106.33	103.00	117.33	106.67	108.33
47	OS-285	110.00	91.33	113.00	101.00	103.83	97.00	94.33	108.67	98.00	99.50
48	OS-286	114.00	85.00	125.00	108.00	108.08	115.33	102.00	120.00	104.00	110.33
49	HJ-8	107.00	85.00	126.00	109.00	106.75	137.00	124.67	145.67	126.33	133.41
50	HFO-114	104.00	87.00	118.00	105.00	103.50	102.67	97.67	95.33	94.00	97.41
	SE	**0.80**	**0.87**	**0.71**	**0.75**	**0.42**	**1.20**	**1.56**	**1.59**	**1.66**	**0.76**

Sr. No.	Genotypes	No. of tillers/plant					Stem diameter (mm)				
		E_1	E_2	E_3	E_4	Pooled	E_1	E_2	E_3	E_4	Pooled
1	Kent	10.67	8.87	8.00	8.20	8.93	8.13	7.00	7.80	6.33	7.31
2	DFO-54	11.80	10.47	8.60	8.23	9.77	8.50	7.30	9.67	8.13	8.40
3	DFO-57	14.13	10.77	7.80	8.00	10.17	7.73	6.67	8.37	7.00	7.44
4	JHO-94-1	11.70	10.57	10.46	9.63	10.59	5.67	5.63	6.10	5.70	5.77
5	JHO-94-3	9.50	7.96	6.00	6.60	7.51	7.70	6.67	9.33	8.33	8.00
6	JHO-95-1	10.70	9.73	7.13	6.80	8.60	8.70	8.63	8.20	7.33	8.22
7	JHO-95-2	11.43	9.73	9.80	9.60	10.14	7.70	5.97	7.40	6.33	6.85
8	JHO-96-4	11.53	9.90	7.87	8.60	9.47	8.83	7.53	9.07	7.36	8.20
9	JHO-96-6	14.47	11.47	8.60	10.10	11.15	7.90	8.53	8.33	7.40	8.04
10	JHO-97-4	15.46	10.47	10.50	10.60	11.75	8.60	6.93	8.06	7.40	7.75
11	JHO-810	13.03	9.73	9.17	11.00	10.73	6.97	7.10	8.00	5.67	6.93
12	JHO-822	15.10	11.07	9.60	10.00	11.44	7.23	7.20	8.40	6.80	7.41
13	JHO-829	13.33	11.97	9.53	13.40	12.05	6.67	6.67	6.70	5.60	6.42
14	JHO-851	15.50	12.90	11.87	13.00	13.31	6.97	5.57	7.67	6.06	6.56
15	JHO-866	12.87	10.40	8.40	8.80	10.11	8.50	8.07	9.33	9.33	8.81
16	JHO-889	14.30	10.60	8.90	7.97	10.44	9.23	8.80	8.40	8.93	8.84
17	JHO-897	12.83	11.00	7.00	10.00	10.20	8.57	8.57	8.86	8.46	8.61
18	JHO-995	14.00	12.46	7.20	8.40	10.51	8.43	8.37	8.43	8.33	8.39
19	JHO-851E	13.77	11.90	9.53	12.70	11.97	7.97	7.43	7.50	6.36	7.31
20	JHO-99-1	12.06	9.50	9.40	12.00	10.74	7.20	6.93	9.13	8.87	8.03
21	JHO-99-2	12.10	10.63	8.17	9.20	10.02	8.37	7.16	8.00	7.33	7.71
22	JHO-99-3	10.43	9.30	5.80	7.60	8.28	6.93	7.66	7.97	7.36	7.48
23	JHO-99-4	9.80	7.40	4.60	6.00	6.95	8.87	8.53	7.83	7.56	8.20
24	JHO-99-5	12.43	9.90	7.53	7.40	9.31	8.53	7.63	8.87	8.66	8.42
25	JHO-99-6	10.77	9.93	8.53	8.60	9.45	8.77	8.40	9.20	8.37	8.68
26	JHO-99-7	14.46	15.00	9.80	12.60	12.96	8.67	8.27	8.73	7.80	8.38
27	Blacknip	9.30	7.90	5.60	4.60	6.85	9.90	9.10	9.20	8.70	9.22
28	S-2688	16.50	11.73	7.20	8.10	10.88	8.87	7.97	7.93	6.03	7.70
29	S-3021	15.93	10.40	7.70	6.43	10.11	8.67	8.37	7.13	6.50	7.66
30	UPO-212	11.70	10.53	8.73	7.80	9.69	8.50	8.07	7.43	7.23	7.80
31	UPO-230	10.63	9.13	5.60	5.20	7.64	8.83	8.73	9.53	8.10	8.79
32	UPO-248	9.33	8.87	6.00	6.40	7.65	8.73	8.73	7.87	7.63	8.24
33	UPO-250	10.40	9.30	7.00	6.20	8.22	8.97	8.67	9.13	7.63	8.60
34	UPO-288	10.93	9.77	6.13	6.63	8.36	7.83	7.43	8.73	7.66	7.92
35	OL-661	13.83	9.23	8.06	9.60	10.18	7.87	6.17	7.50	7.00	7.13
36	OL-805	12.63	9.03	6.83	8.67	9.29	8.17	6.50	7.00	6.67	7.08
37	OL-936	13.40	8.47	6.33	7.80	9.00	8.97	7.30	8.20	7.33	7.95
38	OS-6	12.43	9.90	6.40	6.46	8.80	7.77	7.73	7.33	5.70	7.13
39	OS-7	12.53	9.80	7.10	6.93	9.09	9.33	8.70	9.20	6.97	8.55
40	OS-174	12.10	8.77	7.90	9.00	9.44	8.90	8.50	7.66	6.83	7.97
41	OS-189	10.90	8.40	7.53	7.17	8.50	9.90	9.83	9.73	8.46	9.48
42	OS-237	10.80	9.27	7.46	7.06	8.65	9.70	9.30	9.50	7.70	9.05
43	OS-242	11.00	9.03	7.00	6.06	8.27	8.97	9.30	8.83	7.40	8.62
44	OS-245	9.90	7.20	6.00	5.10	7.05	9.37	8.50	9.63	8.16	8.92
45	OS-277	9.43	8.37	6.80	6.80	7.85	8.33	7.67	7.53	6.77	7.65
46	OS-279	13.10	8.97	9.40	8.80	10.06	8.23	7.80	7.33	4.40	6.94
47	OS-285	12.80	7.50	7.10	7.40	8.70	7.67	7.60	8.17	6.66	7.52
48	OS-286	11.26	6.80	6.50	5.60	7.54	8.67	8.43	7.60	6.77	7.87
49	HJ-8	11.00	10.13	8.53	7.17	9.20	9.90	9.87	9.90	9.33	9.74
50	HFO-114	13.30	12.00	9.13	8.80	10.80	7.80	7.20	7.77	7.33	7.52
	SE	**0.60**	**0.43**	**0.39**	**0.43**	**0.30**	**0.28**	**0.33**	**0.25**	**0.29**	**0.16**

Sr. No.	Genotypes	No. of leaves/plant					Leaf length (cm)				
		E_1	E_2	E_3	E_4	Pooled	E_1	E_2	E_3	E_4	Pooled
1	Kent	50.00	41.66	41.00	39.00	42.91	53.00	45.33	51.66	49.00	49.75
2	DFO-54	60.00	53.00	44.00	42.33	49.83	55.33	54.00	51.66	48.00	52.25
3	DFO-57	71.00	54.00	41.00	41.66	51.91	57.00	56.66	50.66	50.66	53.75
4	JHO-94-1	51.66	46.66	46.00	42.00	46.58	34.67	34.33	35.66	32.33	34.25
5	JHO-94-3	50.00	42.00	35.33	35.00	40.58	46.67	52.33	46.66	47.00	48.16
6	JHO-95-1	59.00	53.66	39.33	38.00	47.50	50.00	49.00	51.00	48.00	49.50
7	JHO-95-2	57.33	48.67	56.00	54.33	54.08	56.00	53.67	52.66	49.33	52.91
8	JHO-96-4	63.66	54.67	42.66	48.00	52.25	51.66	46.33	48.66	46.66	48.33
9	JHO-96-6	91.33	72.33	66.33	55.33	66.33	50.33	51.66	49.00	43.00	48.50
10	JHO-97-4	89.66	60.66	62.66	63.33	69.08	49.00	49.00	49.00	42.66	47.41
11	JHO-810	60.00	45.00	40.00	48.33	48.33	38.66	38.00	36.00	39.66	38.08
12	JHO-822	68.33	50.33	51.66	52.00	55.58	48.33	45.00	58.00	46.00	49.33
13	JHO-829	60.00	54.00	48.33	63.33	56.41	35.33	34.00	34.33	34.33	34.50
14	JHO-851	85.00	77.33	57.67	59.33	69.83	47.33	43.66	49.00	39.00	44.75
15	JHO-866	73.33	59.00	54.33	55.00	60.41	48.00	42.33	46.00	42.33	44.66
16	JHO-889	90.33	67.00	56.33	51.00	66.16	52.33	49.66	44.66	48.33	48.75
17	JHO-897	70.66	61.00	42.00	58.33	58.00	52.00	41.33	45.00	44.33	45.66
18	JHO-995	69.00	61.33	36.00	43.00	52.33	51.66	43.00	44.33	45.33	46.08
19	JHO-851E	75.33	65.00	50.00	67.00	64.33	51.66	47.67	51.33	41.33	48.00
20	JHO-99-1	75.00	59.00	55.67	71.33	65.25	42.00	40.66	42.00	44.33	42.25
21	JHO-99-2	58.00	50.66	43.33	49.33	50.33	44.00	45.00	41.00	44.00	43.50
22	JHO-99-3	58.00	51.33	33.66	43.33	46.58	51.33	50.00	47.00	47.66	49.00
23	JHO-99-4	51.66	39.33	25.67	33.33	37.50	44.66	44.33	48.66	47.33	46.25
24	JHO-99-5	78.33	62.33	43.66	43.00	56.83	51.66	41.00	49.66	43.33	46.41
25	JHO-99-6	61.33	56.67	48.33	48.00	53.58	52.33	49.00	53.00	48.00	50.58
26	JHO-99-7	89.66	92.67	56.00	76.67	78.75	50.66	46.33	47.00	45.67	47.41
27	Blacknip	73.00	60.00	33.66	28.00	48.66	46.00	40.66	44.00	38.33	42.25
28	S-2688	82.66	58.66	36.00	41.00	54.58	55.33	41.33	56.00	45.33	49.50
29	S-3021	84.66	55.33	50.33	42.33	58.16	53.33	48.33	44.00	46.33	48.00
30	UPO-212	63.33	57.00	47.66	44.00	53.00	62.67	51.66	52.33	53.00	54.92
31	UPO-230	59.00	50.66	30.33	28.00	42.00	44.00	43.33	42.66	45.66	43.91
32	UPO-248	55.00	51.33	31.00	34.00	42.83	56.00	49.00	46.00	49.66	50.16
33	UPO-250	60.33	54.00	40.66	36.00	47.75	54.00	48.33	45.00	49.33	49.16
34	UPO-288	56.00	50.00	28.33	32.33	41.66	43.00	53.00	40.66	43.33	45.00
35	OL-661	71.33	46.33	43.33	52.00	53.25	54.33	53.67	52.33	46.00	51.58
36	OL-805	65.66	47.00	40.00	54.00	51.66	52.33	50.67	55.33	43.00	50.33
37	OL-936	73.66	46.66	36.33	46.33	50.75	58.00	55.67	56.33	51.66	55.41
38	OS-6	57.33	44.67	38.66	38.00	44.66	51.00	50.33	45.00	47.66	48.50
39	OS-7	67.66	53.00	41.66	41.33	50.91	53.00	51.66	45.33	48.00	49.50
40	OS-174	62.00	45.00	42.00	47.00	49.00	51.33	48.00	53.33	49.00	50.41
41	OS-189	62.33	48 00	50.33	49.00	52.41	54.00	54.00	52.00	53.00	53.25
42	OS-237	63.00	54.33	46.33	44.00	51.91	55.00	52.33	53.00	50.00	52.58
43	OS-242	66.00	54.33	38.00	33.00	47.83	56.33	55.33	48.33	50.00	52.50
44	OS-245	55.33	39.66	33.66	29.00	39.41	57.33	56.00	53.00	49.00	53.83
45	OS-277	43.33	38.66	32.66	32.66	36.83	56.00	53.00	54.33	48.00	52.83
46	OS-279	65.33	45.66	46.00	43.00	50.00	52.00	44.66	56.66	44.00	49.33
47	OS-285	65.00	38.00	44.66	46.00	48.41	53.00	45.00	52.66	44.66	48.83
48	OS-286	66.00	40.66	35.00	30.66	43.08	57.66	52.33	58.67	47.33	54.00
49	HJ-8	68.00	62.33	49.00	42.00	55.33	55.66	54.00	51.00	52.33	53.25
50	HFO-114	65.00	59.00	47.33	46.66	54.50	55.33	52.00	48.66	45.33	50.33
	SE	**2.33**	**1.65**	**1.69**	**1.75**	**1.09**	**0.96**	**0.93**	**1.02**	**0.92**	**0.80**

Sr. No.	Genotypes	Leaf breadth (cm)					Leaf: stem ratio				
		E_1	E_2	E_3	E_4	Pooled	E_1	E_2	E_3	E_4	Pooled
1	Kent	2.20	2.03	2.03	1.93	2.05	0.34	0.41	0.30	0.38	0.36
2	DFO-54	2.36	2.23	2.67	2.40	2.41	0.33	0.31	0.27	0.28	0.29
3	DFO-57	2.20	2.10	2.47	1.97	2.18	0.44	0.36	0.33	0.36	0.37
4	JHO-94-1	1.90	1.80	1.90	1.50	1.78	0.31	0.23	0.30	0.23	0.27
5	JHO-94-3	2.36	2.30	2.50	2.27	2.35	0.30	0.27	0.26	0.24	0.27
6	JHO-95-1	2.60	2.50	2.50	2.36	2.49	0.29	0.38	0.27	0.32	0.31
7	JHO-95-2	1.90	1.73	2.13	1.77	1.88	0.36	0.39	0.37	0.38	0.37
8	JHO-96-4	2.53	2.03	2.87	2.40	2.45	0.28	0.29	0.27	0.29	0.28
9	JHO-96-6	2.03	1.90	2.20	1.87	2.00	0.39	0.45	0.33	0.43	0.40
10	JHO-97-4	2.07	1.90	2.23	2.03	2.05	0.38	0.43	0.38	0.44	0.41
11	JHO-810	2.03	2.00	2.20	1.73	1.99	0.34	0.37	0.25	0.34	0.32
12	JHO-822	1.83	1.77	2.20	1.90	1.92	0.34	0.35	0.30	0.30	0.32
13	JHO-829	1.87	1.87	1.90	1.93	1.89	0.26	0.30	0.30	0.28	0.28
14	JHO-851	1.90	1.87	2.30	1.83	1.97	0.43	0.44	0.41	0.34	0.40
15	JHO-866	2.53	2.30	2.53	2.30	2.41	0.35	0.38	0.33	0.40	0.36
16	JHO-889	2.77	2.37	2.47	2.40	2.50	0.32	0.34	0.23	0.34	0.30
17	JHO-897	2.57	2.50	2.50	2.26	2.45	0.41	0.38	0.38	0.36	0.38
18	JHO-995	2.43	2.37	2.23	2.23	2.31	0.29	0.36	0.25	0.29	0.30
19	JHO-851E	2.57	2.07	2.10	2.03	2.19	0.43	0.44	0.34	0.33	0.38
20	JHO-99-1	2.30	2.07	2.50	2.13	2.25	0.34	0.39	0.28	0.39	0.35
21	JHO-99-2	2.47	1.97	2.40	2.10	2.23	0.28	0.31	0.32	0.30	0.30
22	JHO-99-3	2.43	2.13	2.43	2.06	2.26	0.34	0.35	0.27	0.32	0.32
23	JHO-99-4	2.57	2.43	2.17	2.13	2.32	0.29	0.27	0.23	0.27	0.27
24	JHO-99-5	2.37	1.80	2.23	2.03	2.10	0.37	0.38	0.35	0.30	0.35
25	JHO-99-6	2.73	2.77	2.70	2.10	2.57	0.39	0.50	0.37	0.48	0.43
26	JHO-99-7	2.50	2.37	2.40	2.36	2.40	0.43	0.40	0.37	0.37	0.39
27	Blacknip	2.87	2.80	2.80	2.43	2.73	0.47	0.61	0.43	0.52	0.50
28	S-2688	2.20	2.17	2.06	1.90	2.08	0.41	0.41	0.32	0.35	0.37
29	S-3021	2.23	2.06	2.07	1.87	2.05	0.40	0.34	0.38	0.50	0.40
30	UPO-212	2.37	2.17	2.23	2.20	2.24	0.42	0.39	0.28	0.38	0.37
31	UPO-230	2.30	2.13	2.40	2.10	2.23	0.33	0.31	0.25	0.26	0.28
32	UPO-248	2.40	2.23	2.10	2.06	2.20	0.34	0.33	0.29	0.39	0.33
33	UPO-250	2.46	2.37	2.30	2.20	2.33	0.30	0.34	0.26	0.27	0.29
34	UPO-288	2.13	2.10	2.07	2.13	2.10	0.27	0.33	0.23	0.25	0.27
35	OL-661	2.17	2.00	2.17	1.93	2.06	0.32	0.36	0.28	0.34	0.32
36	OL-805	2.13	2.00	2.00	1.90	2.01	0.29	0.44	0.30	0.43	0.36
37	OL-936	2.30	2.20	2.33	2.03	2.21	0.27	0.35	0.27	0.37	0.31
38	OS-6	2.06	2.03	2.17	1.80	2.02	0.36	0.34	0.27	0.33	0.32
39	OS-7	2.90	2.80	2.73	2.20	2.65	0.37	0.30	0.29	0.28	0.31
40	OS-174	2.30	2.27	2.33	2.03	2.23	0.39	0.34	0.33	0.31	0.34
41	OS-189	3.03	2.97	2.77	2.70	2.86	0.31	0.38	0.27	0.31	0.31
42	OS-237	2.90	2.83	2.77	2.36	2.71	0.30	0.35	0.26	0.36	0.31
43	OS-242	2.90	2.83	2.60	2.40	2.68	0.35	0.25	0.28	0.28	0.29
44	OS-245	3.03	2.40	2.70	2.43	2.64	0.41	0.37	0.34	0.28	0.35
45	OS-277	2.60	2.20	2.23	1.90	2.23	0.40	0.35	0.33	0.29	0.34
46	OS-279	2.20	2.03	2.23	1.63	2.02	0.35	0.29	0.28	0.22	0.28
47	OS-285	2.56	2.47	2.40	2.03	2.36	0.37	0.34	0.30	0.29	0.32
48	OS-286	2.50	2.30	2.27	2.06	2.28	0.40	0.30	0.34	0.24	0.32
49	HJ-8	2.93	2.87	2.97	2.87	2.91	0.33	0.31	0.27	0.31	0.30
50	HFO-114	2.27	2.07	2.30	2.03	2.17	0.31	0.32	0.31	0.37	0.32
	SE	**0.08**	**0.07**	**0.08**	**0.08**	**0.07**	**0.03**	**0.03**	**0.03**	**0.04**	**0.03**

Sr. No.	Genotypes	Green fodder yield/plant (g)					Dry fodder yield/plant (g)				
		E_1	E_2	E_3	E_4	Pooled	E_1	E_2	E_3	E_4	Pooled
1	Kent	316.00	132.33	224.33	117.00	197.41	57.00	24.00	38.33	21.66	35.25
2	DFO-54	398.66	219.66	318.33	174.00	277.66	87.67	44.33	60.66	38.33	57.75
3	DFO-57	532.34	173.33	258.33	127.00	272.75	95.67	38.33	54.33	29.66	54.50
4	JHO-94-1	210.00	148.00	208.00	136.00	175.50	40.00	31.33	39.67	27.33	34.58
5	JHO-94-3	388.00	171.00	246.66	141.33	236.75	77.67	34.33	49.67	27.00	47.16
6	JHO-95-1	436.33	245.33	280.00	171.00	283.17	91.33	53.67	59.00	37.33	60.33
7	JHO-95-2	274.67	182.33	245.00	172.66	218.66	49.00	34.67	44.33	33.00	40.25
8	JHO-96-4	517.67	248.33	365.67	223.66	338.83	103.33	49.67	73.33	47.00	68.33
9	JHO-96-6	434.00	189.33	236.33	166.33	256.50	86.67	34.00	47.33	30.00	49.50
10	JHO-97-4	443.67	145.67	273.33	154.00	254.16	79.33	26.33	49.67	29.33	46.16
11	JHO-810	300.00	107.67	180.33	116.67	176.16	59.67	20.67	36.33	24.67	35.33
12	JHO-822	573.00	222.00	317.00	155.67	317.00	119.67	47.00	66.66	34.67	67.00
13	JHO-829	281.33	155.67	201.00	176.00	203.50	58.67	31.00	42.66	37.00	42.33
14	JHO-851	351.00	160.67	218.67	151.00	220.33	74.67	32.33	50.33	30.33	46.91
15	JHO-866	386.67	195.67	320.00	164.00	266.58	65.33	39.33	54.33	33.00	48.00
16	JHO-889	554.67	300.00	379.00	237.00	375.17	116.67	60.00	76.00	47.67	75.08
17	JHO-897	501.67	209.67	237.67	140.66	272.41	80.33	50.67	38.00	32.33	50.33
18	JHO-995	543.33	312.33	255.33	206.33	329.33	108.33	62.67	51.33	41.00	65.83
19	JHO-851E	372.00	151.33	217.66	136.66	219.41	78.33	31.67	48.00	30.00	47.00
20	JHO-99-1	458.33	263.33	328.66	264.33	328.66	77.67	50.00	56.00	47.66	57.83
21	JHO-99-2	338.33	150.00	231.66	129.33	212.33	60.67	33.00	42.33	27.33	40.83
22	JHO-99-3	446.00	254.33	208.66	172.00	270.25	93.33	53.00	48.00	36.00	57.58
23	JHO-99-4	398.33	193.33	163.67	155.00	227.58	91.67	38.67	41.00	31.33	50.66
24	JHO-99-5	441.67	218.33	187.67	148.33	249.00	96.67	46.00	41.67	31.33	53.91
25	JHO-99-6	473.00	240.00	296.00	183.33	298.08	85.00	43.00	56.67	33.33	54.50
26	JHO-99-7	465.00	315.33	297.00	221.33	324.66	80.00	57.00	51.00	43.33	57.83
27	Blacknip	481.67	159.33	195.33	74.33	227.66	86.33	31.67	35.33	16.67	42.50
28	S-2688	576.67	165.67	234.00	109.00	271.33	125.33	36.67	51.66	24.33	59.50
29	S-3021	538.67	202.67	259.00	78.00	269.58	97.00	45.00	46.66	17.66	51.58
30	UPO-212	446.67	265.00	260.33	161.33	283.33	93.97	55.33	55.00	34.33	59.58
31	UPO-230	426.67	291.33	235.67	158.33	278.00	89.33	60.66	50.00	33.33	58.33
32	UPO-248	435.67	196.00	184.33	127.33	235.83	91.67	39.33	40.66	25.33	49.25
33	UPO-250	415.67	195.33	279.33	130.66	255.25	83.33	42.66	56.00	29.00	52.75
34	UPO-288	402.67	235.00	197.33	156.66	247.91	80.67	56.33	43.66	38.00	54.66
35	OL-661	515.00	151.00	271.00	153.33	272.58	97.67	26.67	54.33	28.00	51.66
36	OL-805	503.00	218.67	264.67	164.00	287.58	100.33	44.00	53.00	34.66	58.00
37	OL-936	535.67	156.00	234.33	144.00	267.50	117.66	34.33	54.33	33.00	59.83
38	OS-6	421.67	195.33	226.00	126.33	242.33	96.00	38.67	56.33	25.33	54.08
39	OS-7	446.67	267.33	259.67	190.33	291.00	93.67	55.67	57.33	38.33	61.25
40	OS-174	472.67	229.33	281.00	177.66	290.16	99.00	46.33	61.67	35.66	60.66
41	OS-189	598.67	254.00	368.67	205.66	356.75	131.67	48.33	84.67	42.00	76.66
42	OS-237	515.00	325.00	375.00	232.66	366.91	106.67	59.00	79.00	42.33	71.75
43	OS-242	557.33	270.00	300.33	197.00	331.16	116.00	51.33	66.33	37.33	67.75
44	OS-245	463.33	182.67	249.66	123.00	254.66	96.67	40.00	52.66	28.00	54.33
45	OS-277	377.00	185.00	212.00	115.23	222.33	79.00	38.33	44.66	24.33	46.58
46	OS-279	298.33	154.33	243.00	147.33	210.75	65.33	35.00	53.33	34.33	47.00
47	OS-285	382.33	169.00	231.33	163.33	236.50	76.33	37.33	46.67	39.33	49.91
48	OS-286	461.67	148.67	221.33	114.66	236.58	87.67	31.00	42.67	24.00	46.33
49	HJ-8	533.67	328.33	398.67	233.00	373.41	112.33	69.00	85.00	49.67	79.00
50	HFO-114	330.67	181.00	242.33	141.33	223.83	49.67	34.33	36.67	27.00	36.91
	SE	**14.74**	**6.85**	**9.36**	**5.58**	**5.32**	**3.01**	**1.64**	**1.99**	**1.36**	**1.27**

Sr. No.	Genotypes	Crude protein content (%)					IVDMD (%)				
		E_1	E_2	E_3	E_4	Pooled	E_1	E_2	E_3	E_4	Pooled
1	Kent	9.00	8.80	8.80	8.10	8.67	65.10	61.06	67.20	64.80	64.54
2	DFO-54	9.10	8.86	8.83	8.63	8.85	64.50	64.70	65.06	63.26	64.38
3	DFO-57	8.87	8.73	8.46	8.16	8.55	63.97	62.83	62.33	62.90	63.00
4	JHO-94-1	10.03	9.40	10.06	9.30	9.70	70.40	69.40	67.83	61.56	67.30
5	JHO-94-3	8.80	8.60	9.00	8.13	8.63	69.06	66.50	68.36	64.30	67.05
6	JHO-95-1	8.86	9.06	9.10	8.20	8.81	70.00	68.03	70.10	65.00	68.28
7	JHO-95-2	8.57	8.27	9.40	8.70	8.73	66.23	66.13	70.40	66.03	67.20
8	JHO-96-4	8.17	7.60	8.80	8.20	8.19	63.93	65.46	64.06	60.86	63.58
9	JHO-96-6	8.73	8.20	9.27	8.90	8.77	69.20	63.27	71.13	65.00	67.15
10	JHO-97-4	9.20	8.57	10.37	9.86	9.50	72.53	69.80	70.86	66.50	69.92
11	JHO-810	9.03	8.43	9.03	8.00	8.62	60.90	61.26	61.43	59.00	60.65
12	JHO-822	8.90	8.43	9.00	8.90	8.80	69.36	67.00	68.50	60.56	66.35
13	JHO-829	10.77	9.90	10.13	9.53	10.08	65.13	62.67	67.20	59.00	63.57
14	JHO-851	8.26	8.00	7.50	7.33	7.77	61.70	61.06	62.06	61.66	61.62
15	JHO-866	10.43	9.80	10.23	9.06	9.88	70.40	67.27	69.73	60.77	67.04
16	JHO-889	9.43	9.37	9.37	9.10	9.31	67.93	65.87	69.16	65.83	67.20
17	JHO-897	9.13	8.87	9.40	8.97	9.09	67.77	65.00	68.93	63.76	66.36
18	JHO-995	9.70	9.10	9.00	8.60	9.10	66.23	64.00	66.10	65.03	65.34
19	JHO-851E	8.80	8.66	8.50	7.96	8.48	65.90	62.66	62.20	59.00	62.44
20	JHO-99-1	8.93	8.40	8.87	8.93	8.78	64.10	58.90	60.77	58.60	60.59
21	JHO-99-2	9.83	9.30	8.70	8.46	9.07	66.20	61.70	63.23	58.20	62.33
22	JHO-99-3	9.40	9.03	9.53	8.86	9.20	62.53	61.17	61.27	59.76	61.18
23	JHO-99-4	9.10	8.76	9.00	8.26	8.78	62.43	60.13	59.86	59.73	60.54
24	JHO-99-5	9.03	8.83	8.63	8.06	8.64	65.77	61.03	62.06	56.00	61.21
25	JHO-99-6	9.97	9.77	9.43	8.63	9.45	72.50	70.33	72.56	64.86	70.06
26	JHO-99-7	10.43	10.00	10.80	10.13	10.34	74.07	70.67	73.36	66.80	71.22
27	Blacknip	11.40	11.80	11.30	9.93	11.11	73.43	70.40	73.43	67.50	71.18
28	S-2688	7.83	7.83	8.06	8.13	7.96	65.33	66.03	63.53	59.20	63.52
29	S-3021	7.63	7.93	8.57	8.03	8.04	68.56	63.73	67.33	61.63	65.31
30	UPO-212	9.97	9.20	9.43	8.56	9.29	69.30	66.60	68.63	66.53	67.76
31	UPO-230	9.76	9.36	9.86	8.90	9.47	68.63	65.93	68.20	67.76	67.63
32	UPO-248	10.33	9.16	10.70	10.10	10.07	71.07	69.83	68.56	67.33	69.20
33	UPO-250	8.73	8.56	8.46	8.06	8.45	65.53	62.67	62.50	60.76	62.86
34	UPO-288	8.46	8.03	8.23	8.10	8.20	64.76	62.53	61.77	61.00	62.51
35	OL-661	9.50	9.20	8.96	8.40	9.01	62.83	59.37	62.80	59.96	61.24
36	OL-805	8.76	8.46	8.00	8.03	8.31	62.13	60.73	62.80	58.23	60.97
37	OL-936	9.16	8.97	8.50	8.13	8.69	65.66	63.33	63.73	61.56	63.57
38	OS-6	8.20	7.93	8.26	7.86	8.06	65.56	59.93	63.13	61.50	62.53
39	OS-7	8.43	7.77	8.40	8.20	8.20	66.77	66.33	65.53	63.16	65.45
40	OS-174	8.46	8.27	8.96	8.70	8.60	65.76	63.50	65.83	62.00	64.27
41	OS-189	8.73	8.10	8.53	8.13	8.37	66.93	64.13	68.46	61.03	65.14
42	OS-237	8.96	8.40	8.77	8.27	8.60	67.03	65.13	65.40	61.93	64.87
43	OS-242	8.27	8.06	8.50	7.96	8.20	66.26	67.00	65.83	59.53	64.65
44	OS-245	8.37	8.00	8.20	8.13	8.17	63.83	62.60	62.07	60.23	62.18
45	OS-277	8.60	8.33	8.50	8.03	8.36	59.87	59.67	60.00	57.66	59.30
46	OS-279	8.43	8.23	8.33	7.77	8.19	63.53	62.53	63.40	62.40	62.96
47	OS-285	8.83	8.73	9.10	8.40	8.76	60.10	59.53	59.76	54.47	58.46
48	OS-286	9.07	8.73	9.03	8.17	8.75	66.10	64.23	66.63	58.30	63.81
49	HJ-8	11.30	10.77	10.73	9.77	10.64	70.63	68.03	70.16	69.00	69.45
50	HFO-114	8.86	8.40	8.36	7.20	8.20	69.56	66.50	70.83	67.60	68.62
	SE	**0.25**	**0.17**	**0.27**	**0.21**	**0.13**	**1.57**	**1.36**	**1.52**	**1.54**	**0.88**

ABSTRACT

(a)	Title of the thesis	:	Studies on genetic divergence, associations and phenotypic stability of fodder yield and its component characters in oat (*Avena sativa* L.)
(b)	Full name of degree holder	:	Raj Bahadur
(c)	Title of degree	:	Doctor of Philosophy
(d)	Name and address of the Supervisor	:	Dr. R. N. Choubey Principal Scientist (Plant Breeding) and Head, Division of Crop Improvement IGFRI, Jhansi
(e)	Degree awarding university/ institute	:	Bundelkhand University, Jhansi
(f)	Year of award of degree	:	2002
(g)	Major subject	:	Genetics and Plant Breeding
(h)	Total number of pages in thesis	:	121 (95 + x + VI)
(i)	No. of words in the abstract	:	417

The present investigation was conducted at IGFRI, Jhansi and CCS HAU, Hisar, under normal and late sown conditions. Attempts were made to (i) examine the extent of variability and genetic divergence amongst 50 forage oat genotypes of different geographical origin, (ii) the nature of association and direct and indirect effects of different characters on fodder yield, and (iii) identify the differential response of genotypes over the environments and finding out stable genotypes. Observations were recorded for days to 50% flowering, plant height (cm), number of tillers per plant, stem diameter (mm), number of leaves per plant, leaf length (cm), leaf breadth (cm), green and dry fodder yield per plant (g), crude protein content (%) and *in vitro* dry matter digestibility (%).

Analysis of variance revealed substantial amount of variability for various characters in all the environments. Mahalanobis D^2 statistics revealed considerable genetic diversity among the genotypes. The genotypes were grouped into 8 clusters in E_1 and E_2, 9 in E_3 and E_4, while into 10 clusters on pooled basis. The Cluster I composed the maximum 13, 14, 14, 16 and 11 genotypes in E_1, E_2, E_3, E_4 and pooled analysis, respectively, whereas Cluster VIII (E_1, E_2), IX (E_3, E_4) and X (pooled basis) contained single genotype each. There was no association between clustering pattern and eco-geographical distribution of the genotypes.

Genotypic correlations were of higher magnitude as compared to their corresponding phenotypic correlations in most of the character combinations. Green fodder yield was found to be positively and significantly correlated with plant height, stem diameter, number of leaves per plant, leaf length and leaf breadth in all the environments. Path-coefficient analysis revealed that plant height, number of tillers per plant, stem diameter, number of leaves per plant, leaf breadth and leaf length were the most important characters controlling directly to fodder yield and quality in oat.

Significant linear and non-linear components of G x E interactions were recorded for all the traits. Linear portion was higher for days to 50% flowering, plant height, number of tillers per plant, number of leaves per plant, green and dry fodder yield per plant and IVDMD, whereas for stem diameter, leaf length, leaf breadth, leaf: stem ratio and crude protein content had more non-linear portion of G x E interaction. The genotypes, JHO-95-1, JHO-822, JHO-889, OS-189, HJ-8, JHO-99-6, OS-174, OL-805, OS-7 and OS-237 were identified as promising for hybridization on the basis of their genetic divergence, stability and *per se* performance for several traits particularly green and dry fodder yield and their quality.

R.N. Choubey 17/12/02

SUPERVISOR

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HEAD OF THE DIVISION

Raj B.

DEGREE HOLDER